

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Yang, et al.

Appl. No. : 09/921,013

Filed : July 27, 2001

For : NOVEL MICROORGANISM
ISOLATED FROM CHINESE
ELM (ULMUS SP.) AND
PROCESS FOR PREPARING
EXOPOLYSACCHARIDES
BY EMPLOYING THE
MICROORGANISM

Group Art Unit 1638

I hereby certify that this correspondence and all marked attachments are being deposited with the United States Postal Service as first-class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231, on 1/2/78.

20231, on 5/27/03,
(Date)
Paul C. Steinhardt
Paul C. Steinhardt, Real No. 10 R06

Examiner : Vera Aframova

DECLARATION UNDER 37 C.F.R. § 1.132

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I, Young Joo Kim, do hereby declare as follows:

1. I received a Ph.D. in the Department of Chemical Engineering from Rensselaer Polytechnic Institute in 1993. Since 1995, I have been employed in Samsung Advanced Institute of Technology as a Senior Researcher in Kiheung, Korea. A list of my representative publication is attached hereto as Appendix A.

2. I have read the Official Action dated December 27, 2002 and the references cited therein. I respectfully disagree with the Examiner for the reasons set forth below.

3. Along with my co-inventor, I had the bacterial species first referred to as "BSID-805-1" (hereafter referred to as "the Species") submitted to the Korean Collection for Type

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Cultures, which is associated with the Korea Research Institute of Bioscience and Biotechnology (hereafter "KRIBB"), an international depository authority, under accession (deposition) No. KCTC 0687BP on Nov. 3, 1999.

4. As part of their routine, scientists at KRIBB did a taxonomical study of the Species. The results of this study are attached as Appendix B (hereafter "the Study").

5. One part of the Study was a fatty acid analysis performed using the MIDI apparatus. The fatty acid analysis did not show a 100 % match with any known bacterial Species. Indeed, the analysis showed that the Species was only 47% like *Enterobacter sakazakii*. The best match according to this analysis was to *Pseudomonas agglomans*.

6. A second part of the Study compared the Species to the metabolic pathway diagnostics of other known bacteria. The first of these two panels of metabolic pathway diagnostics (API 20 NE) will identify gram-negative non-*Enterobacteriaceae* microorganisms. This first panel showed that the Species had a 93.6% identity with *Aerobacter hydrophylus*. The second of the two panels (API 20 E) identifies species and sub-species of *Enterobacteriaceae* as well as group and species identification of non-fermenting gram-negative bacteria. This second panel found that the Species had a 99.7% likeness with *Enterobacter sakazakii*. It is useful to note that the Species did not react the same way with four of the twenty individual tests that form the second panel. As the results indicate, 100% of the *sakazakii* bacteria react with the nitrate: reduction and oxidation (glucose) tests, while the Species did not react in either such test.

7. The Study also included a 16S ribosomal RNA analysis and comparison with other species. Based on this analysis, two phylogenetic trees were made to illustrate the relation between the Species and other bacteria that had the most similar RNA sequences. As can be seen on page 9 of the Study, the Species is not grouped together in a family with any other known bacteria.

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8. Finally, the Study sets forth on page 10 sets forth a carbon source utilization analysis ("Biolog") for the Species. This analysis is not compared to carbon source utilization analysis of other bacteria.

9. Based on the Study, KRIBB decided that the Species was a novel Species of *Enterobacter*. We named the Species *Enterobacter* sp. SSYL (KCTC 0687BP).

10. My co-inventor and I also subjected the Species to a comparative carbon source utilization test using the Biolog instrument and standard methods. We compared *Enterobacter sakazakii* with the Species and found that for the panel of 96 individual tests in the Biolog analysis, the two organisms gave the opposite results in 51 of the tests. Also, there was some question that the two organisms gave the same results in 20 of the other individual tests. (The read-out for this Biolog test is attached as Appendix C).

11. My co-inventors and I also did a comparative 16S ribosomal RNA analysis on the Species and on the *Enterobacter sakazakii* as wells as on the *Enterobacter cloacae* organisms. (The results of these two analyses are attached as Appendix D and E, respectively). The test showed that the Species had 98% identity with the *Enterobacter sakazakii* microorganism and 94.5% identity with *Enterobacter cloacae* microorganism.

12. The apparent closeness in the 16S ribosomal RNA analysis can be misleading when taken out of context of a full range of taxonomical testing. For instance, a BLAST search of the NCBI database (attached as Appendix F) shows that the in a similar analysis organisms from different genera such as *Citrobacter* (Page 6), *Salmonella* (Page 11) and *Klebsiella* (page 13) have a 97% identity reading with *Enterobacter sakazakii*. Thus, microorganisms can be clearly distinct from one another and have a misleadingly high percentage of identity. The Species is clearly different from either *Enterobacter sakazakii* or *Enterobacter cloacae* as confirmed by the above tests.

13. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that

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these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Respectfully submitted,

Dated: May 26, 2003

By: 
Young Joo Kim

Address: 102-1206 Sejong Apartment
Jemmin-dong, Yuseong-gu,
Taejeon, Republic of Korea

S:\DOCS\MCK\MCK-6690.DOC
120402
S:\DOCS\PCSVCS-3007.DOC
052103



APPENDIX A

A list of Kim Y.J.'s representative publication

Publication

Kim YJ and Cramer SM, "Metal Affinity Displacement Chromatography of Proteins," *J. Chromatography* 549, 89-99 (1991).

Kim YJ, "Preparative Purification of Recombinant Thrombolytic Protein from Complex Biological Mixtures," *Biotechnology Techniques* 8(7), 457-462 (1994).

Kim YJ and Cramer SM, "Experimental Studies in Metal Affinity Displacement Chromatography of Proteins," *J. Chromatography A* 686, 193-203 (1994).

Hrushesky WJM, Langevin T, Kim YJ and Wood PA, "Circadian Dynamics of Tumor Necrosis Factor-alpha (Cachectin) Lethality," *J. Experimental Medicine* 180(3), 1059-1065 (1994).

Vunnum S, Gallant SR, Kim YJ and Cramer SM, "Immobilized Metal Affinity Chromatography: Modeling of Nonlinear Multicomponent Equilibrium," *Chemical Engineering Science* 50(11), 1785-1803 (1995).

Kim YJ, "SCX Separation of Recombinant Thrombolytic Protein from Complex Biological Feeds," *Biotechnology Techniques* 9(6), 417-422 (1995).

Kim SJ, Jang YC, Kil SG and Kim YJ, "Temperature Change Inside a Rubber Sheet During the Process of Heating and Cooling," *Polymer(Korea)* 19(2), 213-222 (1995).

Kim YJ, "Modeling of Non-Ideal Displacement Separation in Immobilized Metal Ion Affinity Chromatography," *Biotechnology Techniques* 9(9), 623-628 (1995).

Kim YJ, "Prediction of Protein Displacement by Simplified Immobilized Metal Ion Affinity Chromatographic Model," *Bioseparation* 5, 295-306 (1995).

Kim YJ, "Optimized Operating Parameters for the Displacement Separation of Biomolecules in Immobilized Metal Ion Affinity Chromatography," *Biotechnology Techniques* 13(12), 837-842 (1999).

Yang CS, Kim JS, Choi JW, Kwon MH, Kim YJ, Choi JG and Kim GT, "XPS Study of Aluminum Oxides Deposited on PET Thin Film," *Journal of Industrial and Engineering Chemistry* 6(3), 149-156 (2000).

Yang YL, Kim YJ, Kim KH and Oh E, "Separation of glycoprotein and its anticancer immunostimulating activity from dried barks of slippery Elm (*Ulmus parvifolia*)," *Korean J. Biotechnol. Bioeng.* 16(6), 547-553 (2001).

Yang YL and Kim YJ, "Immunostimulating exopolysaccharide with anticancer activity from *Enterobacter* sp. SSYL(KCTC 0687BP) screened from *Ulmus parvifolia*" *Korean J. Biotechnol. Bioeng.* 16(6), 554-561 (2001).

Books

Kim SJ, Kim JH and Kim YJ, "Unit Operations," *DongHwa KiSeul Publications*, ISBN 89-425-0502-3, pp 384, Korea, 1996.

Kim KY, No SY and Kim YJ, "New Combustion Engineering," *DongHwa KiSeul Publications*, ISBN 89-425-2404-4, pp 314, Korea, 1997.

Patents

Oh E, Kim YJ and Park HG, "Development of complex oral slow-release drug delivery system using alginate-polysaccharide beads", *Korea Patent* 245773 (Dec. 1, 1999), *Korea Patent* filing number 97-31780 (July 9, 1997).

Yang YL, Kim YJ, Kim KH and Oh E, "Peptido-glyco compounds separated from Slippery Elm for anticancer immunoactive material and the processes for the preparation of the material", *Korea Patent* 348870 (Aug. 1, 2002), *Korea Patent* filing number 2000-636 (Jan. 7, 2000).

Yang YL and Kim YJ, "Production of immunostimulating exopolysaccharide with anticancer activity from *Enterobacter* sp. SSYL (KCTC 0687BP) screened from *Ulmus parvifolia*," *Korea Patent* filing number 2000-43675 (July 28, 2000).

Yang YL and Kim YJ, "A Novel Microorganism Isolated from Chinese Elm (*Ulmus* Sp.) and Process for Preparing Exopolysaccharides by Employing the Microorganism," *US Patent* filing number 09/921,013 (July 27, 2001).

Kim YJ and Park KH, "Probe design methods for the detection of neighboring SNPs or nucleotide sequence mutations" *Korea Patent* filing number 2001-75283 (Nov. 30, 2001).

Kim YJ and Park KH, "Scoring and selection for optimum probes in probes design" *Korea Patent* filing number 2001-79722 (Dec. 15, 2001).

Kim YJ, Song MJ and Shim HS, "Method for detecting a defect in a microarray" *Korea Patent* filing number 2002-65521 (Oct. 25, 2002).

APPENDIX B

Fatty Acid Analysis Result Report

첨가물 1. 균체지방산 분석 결과 보고서

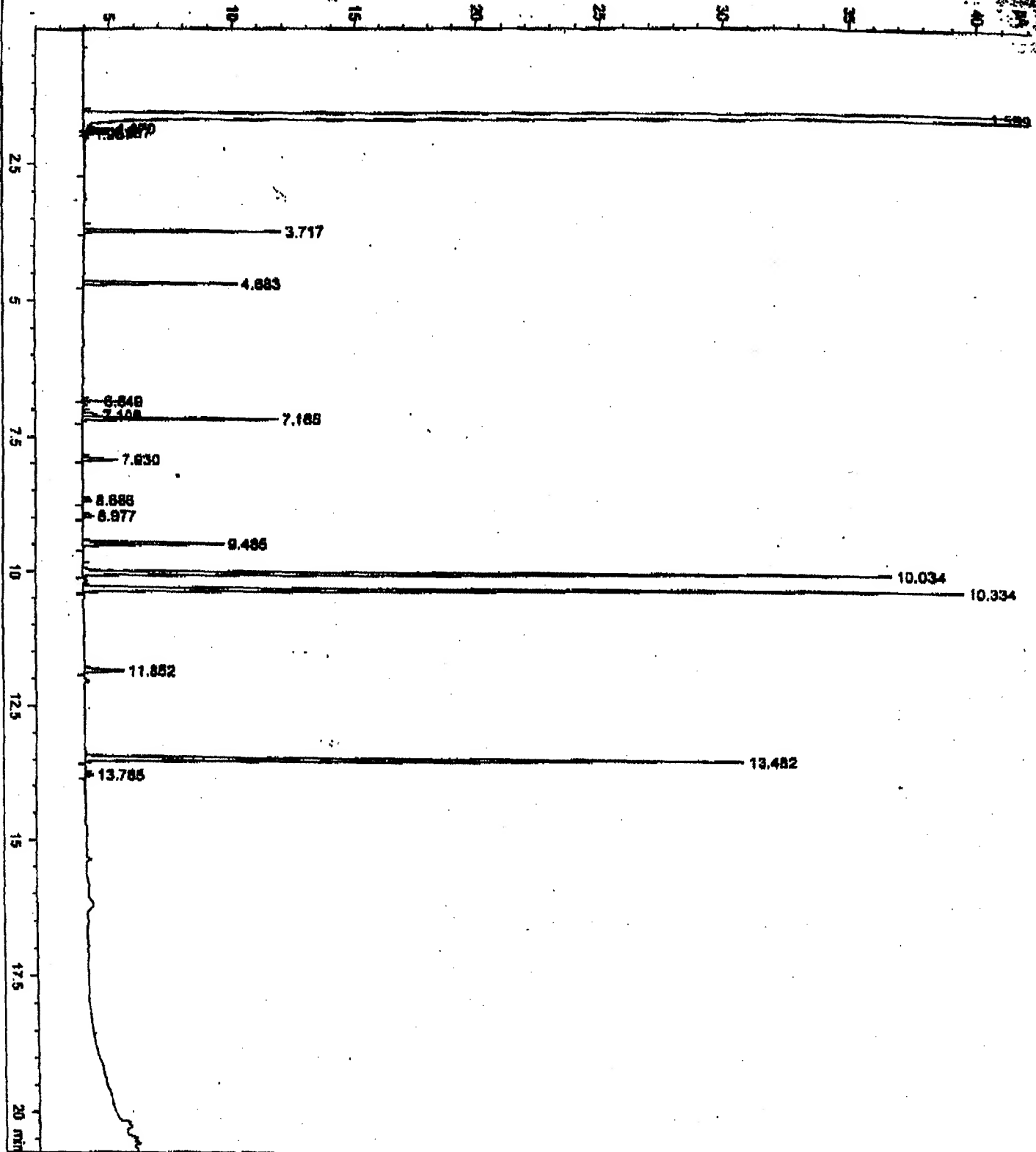
균주번호	접수번호 (BSID)
	807-1, 2

● RESULTS

BSID-805-1, 2의 균체지방산 분석 결과를 첨부합니다. 의뢰균주는 MIDI 데이터 베이스의 균주들과 비교했을 때, Enterobacteriaceae family의 균주들과 가까운 것으로 분석되었습니다. API나 BIOLOG 결과와 비교하는 것이 좀 더 정확한 동정에 접근할 것으로 생각합니다.

1999년 1월 6일

균체지방산 분석 담당 이정숙/이근철



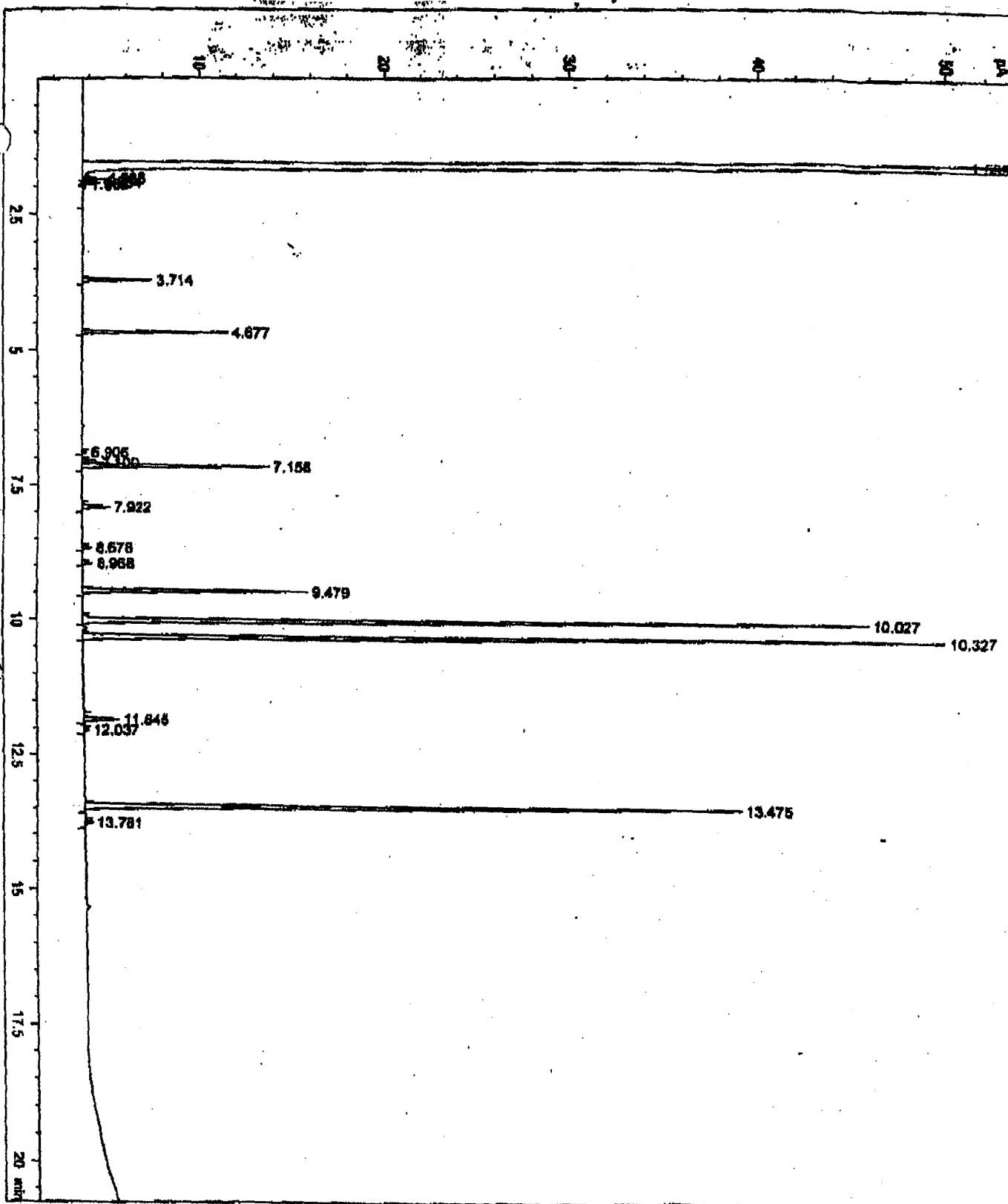
* * End f Rep rt ***

ID: 344 BSTD-807-1 (ANALYSIS) Date of run: 06-JUN-99 14:02:41
 Bottle: 12 SAMPLE

RT	Area	Area/RT	Response	ECI	Name	Q	Comment 1	Comment 2
1.889	435067406	0.027		7.008	SOLVENT PEAK		< min rt	
1.878	3719	0.028		7.332			< min rt	
1.937	2474	0.021		7.806			< min rt	
1.967	343	0.019		7.747			< min rt	
3.717	28348	0.025	1.108	10.918	Sum In Feature 3	4.58	ECI deviates 0.004	12:0 ALDH ?
4.693	22761	0.029	1.048	13.000	12:0	3.87	ECI deviates 0.000	Reference 0.009
6.648	528	0.008		13.766			< min area/rt	
7.108	4289	0.042	0.978	13.857	unknown 13.861	0.68	ECI deviates -0.004	
7.148	35933	0.036	0.977	13.899	14:0	5.70	ECI deviates -0.001	Reference 0.007
7.930	6995	0.038	0.968	14.802	unknown 14.803	1.10	ECI deviates -0.001	
8.686	1944	0.040	0.988	15.000	15:0	0.30	ECI deviates -0.000	Reference 0.007
8.977	3891	0.039		15.176				
9.468	29827	0.040	0.948	15.486	Sum In Feature 3	4.59	ECI deviates 0.004	16:1 ISO I/14:0 30H
10.034	171829	0.041	0.943	15.819	Sum In Feature 4	26.33	ECI deviates 0.002	16:1 w7a/15 iso 30H
10.334	186332	0.041	0.941	16.001	16:0	28.48	ECI deviates 0.001	Reference 0.008
11.852	8971	0.042	0.933	16.888	17:0 C10H8	1.38	ECI deviates 0.000	Reference 0.006
13.482	180723	0.044	0.929	17.828	Sum In Feature 7	22.74	ECI deviates 0.001	18:1 w9a/w12t/w7a
13.785	1880	0.046	0.928	17.999	18:0	0.38	ECI deviates -0.001	Reference 0.004
*****	58175				unknown 18.228			unknown 18.228
*****							16:1 ISO I/14:0 30H	14:0 30H/16:1 ISO I
*****	171829				unknown 18.228		16:1 w7a/15 iso 30H	15:0 ISO 30H/16:1 w7a
*****	150723				unknown 18.228		18:1 w7a/w12t/w12t	18:1 w9a/w12t/w7a
*****							18:1 w12t/w8t/w7a	

Solvent Area	Total Area	Named Area	% Named	Total Area	Now Ref	ECI Deviation	Ref ECI Shift
435067406	649629	648812	99.57	615687	6	0.002	0.007

TARA (Rev 3.90) Pantecan		0.893	(with. agglomerans, Erwinia herbicola)
P. agglomerans		0.893	(with. agglomerans, Erwinia herbicola)
P. ananas		0.807	(Erwinia ananas)
Salmonella		0.737	
S. typhimurium		0.737	
S. C. CC subgroup A		0.737	
S. typhi		0.507	(confirm with other tests)
S. choleraesuis		0.448	
S. n. choleraesuis		0.448	
Enterobacter		0.704	(excludes ATCC 35549 which is atypical)
E. cloacae		0.704	(excludes ATCC 35549 which is atypical)
E. taylorae		0.694	
E. sakazakii		0.448	
CLIN (Rev 3.90) Citrobacter		0.564	
C. diversus		0.564	
C. amalonitius		0.287	
Enterobacter		0.541	
E. cloacae		0.541	
E. C. CC subgroup A		0.541	
Escherichia		0.516	
E. hesnerii		0.516	
E. coli subgroup B		0.291	(high DNA homology with Shigella)



* End of Report ***

[REDACTED]

Solvent Ar	Total Area	Masked Area	% Masked	Total Amt	Mask Amt	ECI Deviation	Mask ECI Whisk
438884781	844886	844907	99.96	810129	7	0.002	0.002

CLIN [Rev 3.90]	Organism	Value	Notes
	<i>Y. agglomerans</i>	0.894	(Kntb. agglomerans, Erwinia herickella)
	<i>Y. ananatis</i>	0.894	(Kntb. agglomerans, Erwinia herickella)
	<i>Y. ananatis</i>	0.507	(Erwinia ananatis)
	<i>Y. agglomerans</i>	0.732	
	<i>Y. agglomerans</i>	0.732	
	<i>Y. agglomerans</i>	0.732	
	<i>Y. agglomerans</i>	0.489	(confirm with other tests)
	<i>Y. agglomerans</i>	0.481	
	<i>Y. agglomerans</i>	0.481	
	<i>Y. agglomerans</i>	0.729	(excludes ATCC 35549 which is atypical)
	<i>Y. agglomerans</i>	0.729	(excludes ATCC 35549 which is atypical)
	<i>Y. agglomerans</i>	0.702	
	<i>Y. agglomerans</i>	0.470	
	<i>Y. agglomerans</i>	0.551	
	<i>Y. agglomerans</i>	0.551	
	<i>Y. agglomerans</i>	0.515	
	<i>Y. agglomerans</i>	0.515	
	<i>Y. agglomerans</i>	0.509	
	<i>Y. agglomerans</i>	0.509	
	<i>Y. agglomerans</i>	0.288	(high DNA homology with Shigella)

Refer no: 07NE

Date: 02/23/199

GOOD IDENTIFICATION

Strip : API 20 NE

V6.0

Read on: 02/23/199

Profile : 7 5 6 7 7 4 1

NO3 + TRP + GLU + ADH + URE - ESC + GEL - PNPG+ GLUa+ ARa+ MNEa+
MANa+ NAGa+ MALa+ GNTa+ CAPa- ADIa- MLTa+ CITa+ PACa- OX -

----- Significant taxa ----- % Id. --- T -- Tests against -----

Aer.hydro./caviae 93.6 0.33 3

Next choice

Chryseomonas luteola 6.2 0.19 3

POSSIBILITY OF *Vibrio fluvialis*

Aer.hydro./caviae : 3 test(s) against

GELATINE (HYDROLYSE) (GEL) 97 % CAPRATE (ASSIMILATION) (CAPa) 84
OXYDASE (OX) 99 %

Next choice

Chryseomonas luteola : 3 test(s) against

INDOLE (TRP) 0 % GLUCOSE (GLU) 13
N-ACETYL-GLUCOSAMINE (AS (NAGa) 12 %

COMPLEMENTARY TESTS :

GLUCOSEg 0/129 R

Aeromonas caviae	:	2 %	+
Vibrio fluvialis	:	0 %	-
Aeromonas hydrophila	:	94 %	+

Ref rence : 807E

Date : 02/23/195

DOUBTFUL PROFILE

Strip : API 20 E

V4.0

Read on: 02/23/195

Profile : 3 3 4 5 1 7 3 4 5

ONPG+ ADH + LDC - ODC + CIT + H2S - URE - TDA - IND + VP + GEL -
GLU + MAN + INO - SOR - RHA + SAC + MEL + AMY + ARA + OX - NO2 -
N2 - MOB + McC + OF/O- OF/F+

----- Significant taxa ----- % Id. --- T -- Tests against -----

Ent.sakazakii 99.7 0.18 4

Next choice
Ent.amnigenus 1 0.1 0.00 4

POSSIBILITY OF Enterobacter cloacae

Ent.sakazakii : 4 test(s) against

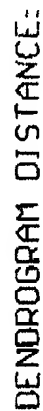
INDOLE (IND) 25 % myo-INOSITOL (INO) 75
NITRATE:REDUCTION EN NO(NO2) 100 % OXYDATION (GLUCOSE) (OF/O) 100

Next choice
Ent.amnigenus 1 : 4 test(s) against

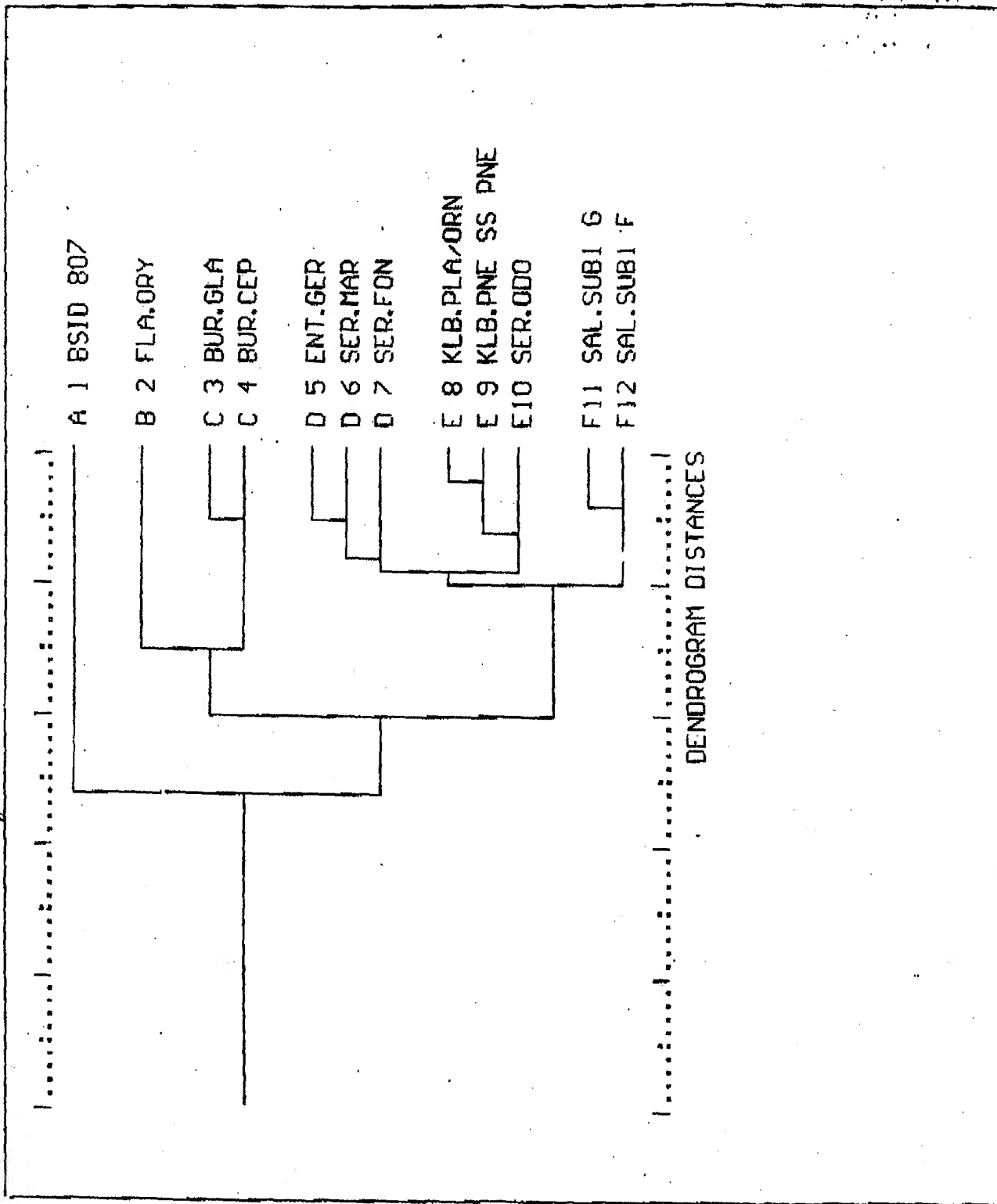
ARGININE DIHYDROLASE (ADH) 25 % INDOLE (IND) 0
NITRATE:REDUCTION EN NO(NO2) 100 % OXYDATION (GLUCOSE) (OF/O) 100

COMPLEMENTARY TESTS :

	YELLOW	ESC (HYD.)
Enterobacter cloacae	0 %	30 %
Ent.sakazakii	98 %	100 %



801) clinical Blood Chemistry



water	α-cyclodextrin	dextrin	glycogen	trex 40	trex 80	N-acetyl-D-Galactosamine	N-acetyl-D-glucosamine	adenitol	L-arabinose	D-arbitol	cellulose
-	-	+	+	-	-	+	+	+	+	+	-
D-erythritol	D-fructose	L-fructose	D-glucose	gentiobiose	α-D-glucose	m-inositol	α-D-lactose	lactulose	malinac	D-mannitol	D-mannose
-	-	+	+	+	-	+	+	+	+	+	+
D-melibiose	β-acetyl-D-glucoside	D-psitose	D-raffinose	L-rhamnose	D-sorbitol	sucrose	D-archibiose	lunrose	xylitol	acetyl pyruvate	mono-acetyl succinate
+	+	+	+	+	+	+	+	+	+	+	+
acetic acid	citric acid	citric acid	fumaric acid	D-galactonic acid lactone	D-galactonic acid	D-gluconic acid	D-glucosaminic acid	D-glucuronic acid	α-hydroxybutyric acid	β-hydroxybutyric acid	γ-hydroxybutyric acid
+	-	-	-	-	-	+	+	+	+	+	+
P-hydroxy phenylacetic acid	itaconic acid	α-keto butyric acid	α-keto glutaric acid	α-keto valeric acid	D,L-lactic acid	malonic acid	propionic acid	quinic acid	D-saccharic acid	sorbic acid	succinic acid
-	+	+	+	-	+	+	+	+	+	+	+
hydro succinic acid	succinamic acid	glucosaminid	alaninamide	D-alanine	L-alanine	L-alanyl-glycine	L-asparagine	L-aspartic acid	L-glutamic acid	glycyl-L-aspartic acid	glycyl-L-glutamic acid
+	+	+	+	+	+	+	+	+	+	+	+
L-Alisidine	hydroxy L-proline	L-leucine	L-orakline	L-phenylalanine	L-proline	L-pyroglutamic acid	D-serine	L-serine	L-threonine	D,L-cantiline	γ-amino butyric acid
+	+	+	+	+	+	+	+	+	+	+	+
Uronic acid	inosine	uridine	thymidine	phenyl ethylamine	putrescine	2-amino ethanol	2,3-bisacetal	glycerol	D,L-α-glycerol phosphate	glucose-1-phosphate	glucose-6-phosphate
+	+	+	+	+	+	+	+	+	+	+	-

2 12/02/98 24 BSD 807 807 ? GN TSA/BUGM
BIO-NUMBER: 1 4 5 6 1 6 4 0 7 7 7 7 4 0 4 0 3 5 7 7 7 7 7 7 7 7 7 6

BEST ID: BURKHOLDERIA CEPACIA

BUR.CEP 0.003 24.085 1.375 3.713

BUR.GLA 0.003 24.337 0.750 4.963

SAL.SUBIF 0.002 25.327 0.958 4.325

0.204 0.214 1.067 1.431 0.204 0.188 0.535 0.178 0.912 1.099 1.498 0.185
0.224 0.179 0.369 1.104 0.395 0.208 0.645 0.166 0.290 0.165 0.179 0.239
0.948 0.871 0.912 0.974 1.475 1.084 1.308 0.997 0.537 0.913 0.505 0.631
0.794 0.187 0.180 0.226 0.232 0.199 1.453 0.176 0.221 0.187 0.173 0.307
0.251 0.620 0.558 1.696 0.230 1.720 1.774 1.112 0.912 1.487 1.683 1.021
1.321 0.879 0.675 1.217 2.050 2.134 0.944 0.796 1.812 1.109 1.942 1.737
1.742 1.960 1.584 1.020 1.095 0.917 1.975 0.965 1.715 0.861 2.109 0.653
1.820 0.723 1.899 0.915 1.936 0.741 1.102 1.037 1.131 1.157 0.707 0.245

0 5 423 601 0 -8 162 -13 347 439 634 -9
10 -12 81 441 94 2 216 -19 42 -19 -12 17
365 327 347 377 623 431 541 389 163 348 148 209
289 -8 -12 11 14 -2 612 -14 8 -8 -15 50
23 204 174 731 13 743 770 445 347 629 725 400
548 331 231 497 905 946 363 290 788 444 852 751
754 861 676 400 437 350 868 373 741 322 929 220
792 254 831 349 849 263 440 408 454 467 247 20

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APPENDIX C

첨부자료 3 : BIOLOG DATA

BIOLOG DATA

water	α-cyclodextrin	dextrin	glycogen	tween40	tween80	N-acetyl-D-Galactosamine	N-acetyl-D-glucosamine	adonitol	L-arabinose	D-arabitol	cellobiose
-(-)	-(-)	+	v(+)	v(-)	-(-)	v(+)	+	-(-)	+	-(-)	+
i-erythritol	D-fructose	L-fucose	D-galactose	gentiobiose	α-D-glucose	m-inositol	α-D-lactose	lactulose	maltose	D-mannitol	D-mannose
-(-)	+	v(+)	+	+	-(-)	-(-)	+	+	+	+	+
D-melibiose	β-methyl D-glucoside	D-psicose	D-raffinose	L-rhamnose	D-sorbitol	sucrose	D-trehalose	turanose	xylitol	methyl pyruvate	mono-methyl succinate
+	+	v(+)	+	v(+)	-(-)	+	+	+	-(-)	-(-)	-(-)
acetic acid	cis-aconitic acid	citric acid	formic acid	D-galactonic acid lactone	D-galacturonic acid	D-gluconic acid	D-glucosaminic acid	D-glucuronic acid	α-hydroxy butyric acid	β-hydroxy butyric acid	γ-hydroxy butyric acid
v(+)	+	+	v(-)	+	+	+	v(-)	+	-(-)	-(-)	-(-)
p-hydroxy phenylacetic acid	itaconic acid	α-keto butyric acid	α-keto glutaric acid	α-keto valeric acid	D,L-lactic acid	malonic acid	propionic acid	quinic acid	D-saccharic acid	sebacic acid	succinic acid
-(-)	-(-)	-(-)	-(-)	-(-)	v(+)	-(-)	-(-)	-(-)	-(-)	-(-)	v(+)
bromo succinic acid	succinamic acid	glucuronamide	alaninamide	D-alanine	L-alanine	L-alanyl-glycine	L-asparagine	L-aspartic acid	L-glutamic acid	glycyl-L-aspartic acid	glycyl-L-glutamic acid
-(-)	-(-)	v(+)	-(-)	-(-)	-(-)	v(+)	+	v(+)	-(-)	-(-)	-(-)
L-histidine	hydroxy L-proline	L-leucine	L-ornithine	L-phenyl alanine	L-proline	L-pyroglutamic acid	D-serine	L-serine	L-threonine	D,L-camitine	γ-amino butyric acid
-(-)	-(-)	-(-)	v(+)	-(-)	v(+)	-(-)	-(-)	+	-(-)	-(-)	-(-)
Urocanic acid	inosine	uridine	thymidine	phenyl ethylamine	putrescine	2-amino ethanol	2,3-butanediol	glycerol	D,L-α-glycerol phosphate	glucose-1-phosphate	glucose-6-phosphate
-(-)	+	v(+)	v(+)	-(-)	-(-)	-(-)	-(-)	+	v(+)	-(-)	-(-)

Control: *Enterobacter sakazaki* () : Screened Cell

전기 BIOLOG DATA 는 인용문헌 1 에 개시된 균주 *Enterobacter sakazakii* 와 본원발명의 균주인 *Enterobacter sp.* SSYL(KCTC 0687BP)가 생존에 이용할 수 있는 물질을 측정하여 비교한 결과로서, ()의 내측에 기재된 결과는 본원발명의 균주를 대상으로 한 DATA 이고, ()의 외측에 기재된 결과는 인용문헌 1 에 개시된 균주를 대상으로 한 DATA 입니다. 전기 BIOLOG DATA 에서 보듯이, 본원발명의 균주와 인용문헌 1 에 개시된 균주는 테스트된 물질의 약 26% 정도에 대하여서만 동일한 결과를 나타내므로, 각 균주의 생존조건이 서로 상이함을 알 수 있습니다.

APPENDIX D

첨부자료 2: 인용문헌 1 의 균주에 대한 rRNA sequence 의 비교분석 자료

16S ribosomal RNA sequence data from *Enterobacter* sp. SSYL deposited under accession number KCTC 0687BP

```

ATTGAACGCTGGCGCAGGCCTAAACACATGCAAGTCGGGGGTAGCACAGGAGCTTGCTCCCGGTGACGAGCGGGACGGGTGAGTAATGTCT
GGGAAACTGCTGATGAGGGGGATAACTACTGGAACCGGTAGCTAATACCGCAIAACGTCTTCGGACCAGTGGGGGACCTTCGGGCCTCATGCC
ATCAGATGTGCCAGATGGGATTAGCTAGTAGGTGGGTAAAGGCTCACCTAGCGACGATCCCTAGCTGCTGAGAGGATGACCCAGCCACACT
GGAAGTGAACACGCTCCAGACTCTACGGAGGCAGTAGGGGAATATTGCATGGCGCAAGCCTGATGCAGCCATGCCGCTGTATGAAG
AAGGCCTTCGGGTGTAAAGTACTTTCAGCGAGGAGGAAGGTGTGTGGTTAATAACACAGCAATTGACGTTACTCGCAGAAAGACACCGGCTA
ACTCCGTGCCAGAGCCGGGTAAATACGGAGGTGCAAGCGTTAATCGGAATTACTGGCGTAAAGCGCACGCGGCTTGTAAAGTCAGATGT
GAAATCCCGGGCTCAACCTGGGAACCTGCAAGCTTGAGTCTCTGAGAGGGGTAGAATCCAGGTGTAGCGGTGAAATGCGT
AGAGATCTGGAGGAATACCGGTGGGAAGCGGCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATTAGATACC
CTGGTAGTCCACGCCGTAAACGATGTGCACTTGGAGGTTGTCCCTTGAGCGTGGCTTCCGAGCTAACCGCTTAAGTCGACCCCTGGGAGTAC
GGCGCAAGGTTAAACTCAATGAATTGACGGGGGCCACAAAGCGGTGGAGCACTGTGATGCAAGCTGCTGATGCAACCGGAAGAACCTTACCTGTT
CTTGACATCCAGAGATCCTGCAGAGATGGGGAGTGCCCTTCGGGAACCTTGAGACAGGTGCTGATGGCTGCTCAGTGGTGAATAACCGGAGGAA
GGTTAAGTCCCGCAACGAGCAACCTTATCTTTTGCCAGCACAGTAAATGGTGGAACTCAAGGAGACTGCCGTGATAAACCGGAGGAA
GGTGGGATGACGTCAAGTCATCATGCCCCCTTACGACCGGCTACACAGTGTACATGGCGCATACAAAGAGACGACTCTCGCGAGAGCAA
GCGGACCTCATAAAGTCGCTGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGTAGTAATCGTAGATCAGAATGCCACGGT
GAATACGTTCCCGGCCTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAGTAGTAGCTTAACCTTCGGGAGGGCGCTTACC
ACTTGTGATTCACTGGGGTG

```

<염기서열 상동성 조사 결과>

<http://www.ncbi.nlm.nih.gov>에서 Blast 를 사용하여 sequence homology 를 조사한 결과 *Enterobacter sakazakii* 균주와 98% homology 를 보이는 것으로 나타났다.

Enterobacter sakazakii gene for 16S ribosomal RNA, partial sequence Length = 1449

Score = 2617 bits (1320), Expect = 0.0
 Identities = 1424/1453 (98%), Gaps = 8/1453 (0%)
 Strand = Plus / Plus

KCTC 0687BP : 6 acgtggcggcaggccctaacacatgcaagtcggcggtagcacaggagc---ttgctcc 62
 |||||
 E. sakazakii: 1 acgtggcggcaggccctaacacatgcaagtcgaacggt---acaggagcagcttgctgc 58
 |||||

KCTC 0687BP : 63 -cgggtgacgagcggcgacgggtgagtaattgtctgggaaactgccctgatggaggggat 121
 ||
 E. sakazakii: 59 tctgctgacgagtgccggacgggtgagtaattgtctgggaaactgccctgatggaggggat 118
 |||||

KCTC 0687BP : 122 aactactggaacggtagctaataccgcataaacgtcttcggaccaagtggggaccttc 181
 |||||
 E. sakazakii: 119 aactactggaacggtagctaataccgcataaacgtctacggaccaagtggggaccttc 178
 |||||

KCTC 0687BP : 182 gggcctcatgccatcagatgtgcccagatgggattagctagtaggtgggtaaggctca 241
 |||||
 E. sakazakii: 179 gggcctcatgccatcagatgtgcccagatgggattagctagtaggtgggtaacggctca 238
 |||||

KCTC 0687BP : 242 cctaggcgacgatccctagctggtctgagaggatgaccagccactggaactgagacac 301
 |||||
 E. sakazakii: 239 cctaggcgacgatccctagctggtctgagaggatgaccagccactggaactgagacac 298
 |||||

KCTC 0687BP : 302 ggtccagactcctacggaggcagcagtgggaatatatgcacaatggcgcaagcctgat 361
|||||
E. sakazakii: 299 ggtccagactcctacggaggcagcagtgggaatatatgcacaatggcgcaagcctgat 358

KCTC 0687BP : 362 gcagccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcgaggagg 421
|||||
E. sakazakii: 359 gcagccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcgaggagg 418

KCTC 0687BP : 422 aaggtgttgtggttaataaccacagcaattgacgttactcgcagaagaagcaccggctaa 481
|||||
E. sakazakii: 419 aaggtgttgtggttaataaccgcagcaattgaogttacccgcagaagaagcaccggctaa 478

KCTC 0687BP : 482 ctccgtgccagcagccgcggttaatacggagggtgcgaagcgttaatcgggaattactggcg 541
|||||
E. sakazakii: 479 ctccgtgccagcagccgcggttaatacggagggtgcgaagcgttaatcgggaattactggcg 538

KCTC 0687BP : 542 taaagcgacgcagcggttgtttaagtcagatgtgaaatccccgggctcaacctgggaa 601
|||||
E. sakazakii: 539 taaagcgacgcagcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaa 598

KCTC 0687BP : 602 ctgcatttgaaactggcaagcttgagctctgtagagggggtagaattccaggtgtagcg 661
 |||||
 E. sakazakii: 599 ctgcatttgaaactggtcagcttgagctctgtagagggggtagaattccaggtgtagcg 658

KCTC 0687BP : 662 gtgaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagac 721
 |||||
 E. sakazakii: 659 gtgaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagac 718

KCTC 0687BP : 722 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc 781
 |||||
 E. sakazakii: 719 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc 778

KCTC 0687BP : 782 cgtaaacgatgtcgacttgaggttgtgcccttgaggcgtggcttcggagctaaccgct 841
 |||||
 E. sakazakii: 779 cgtaaacgatgtcgacttgaggttgtgcccttgaggcgtggcttcggagctaaccgct 838

KCTC 0687BP : 842 taagtcgaccgcctggggagtagcgccgcaaggttaaactcaaatgaattgacgggggc 901
 |||||
 E. sakazakii: 839 taagtcgaccgcctggggagtagcgccgcaaggttaaactcaaatgaattgacgggggc 898

KCTC 0687BP : 902 cgcacaagcgggtggagcatgtggtttaattcgatgaacgcgaagaaccttacctggtc 961
|||||
E. sakazakii: 899 cgcacaagcgggtggagcatgtggtttaattcgatgaacgcgaagaaccttacctggtc 958
|||||

KCTC 0687BP : 962 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1021
|||||
E. sakazakii: 959 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
|||||

KCTC 0687BP : 1022 ctgcatggctgtcgtcagctcgtgtgtgaaatgttgggttaagtcocgcaacgagcgca 1081
|||||
E. sakazakii: 1019 ctgcatggctgtcgtcagctcgtgtgtgaaatgttgggttaagtcocgcaacgagcgca 1078
|||||

KCTC 0687BP : 1082 acccttatacctttgttgcagcacgtaatggtgggaactcaaaggagactgccggtgata 1141
|||||
E. sakazakii: 1079 acccttatacctttgttgcagc-ggttcggccgggaactcaaaggagactgccggtgata 1137
|||||

KCTC 0687BP : 1142 aaccggaggaagtggggatgacgtcaagtcacatggcccttacgaccagggctacaca 1201
|||||
E. sakazakii: 1138 aaccggaggaagtggggatgacgtcaagtcacatggcccttacgaccagggctacaca 1197
|||||

KCTC 0687BP : 1202 cgtgctacaatggcgcatataaagagaagcgactctcgagagcaagcgacctcataa 1261
|||||
E. sakazakii: 1198 cgtgctacaatggcgcatataaagagaagcgac-ctcgagagcaagcgacctcataa 1256

KCTC 0687BP : 1262 agtgcgtcgtagtccggattggagctcgcaactcgactccatgaagtcggaatcgctagt 1321
|||||
E. sakazakii: 1257 agtgcgtcgtagtccggattggagctcgcaactcgactccatgaagtcggaatcgctagt 1316

KCTC 0687BP : 1322 aatcgtggtatcagaatgccacggtgaatacgttcccgggccttgtacacacgcccgctca 1381
|||||
E. sakazakii: 1317 aatcgtggtatcagaatgccacggtgaatacgttcccgggccttgtacacacgcccgctca 1376

KCTC 0687BP : 1382 caccatgggagtggttgcaaaagaagtaggtagcttaacctcgggagggcgcttacca 1441
|||||
E. sakazakii: 1377 caccatgggagtggttgcaaaagaagtaggtagcttaacctcgggagggcgcttacca 1436

KCTC 0687BP : 1442 ctttgtgattcat 1454
|||||
E. sakazakii: 1437 ctttgtgattcat 1449

APPENDIX E

첨부자료 4 : 인용문헌 2 의 균주에 대한 rRNA sequence 의 비교분석 자료

AF511434. *Enterobacter cloacae* [gi:21327114] from NCBI

16S ribosomal RNA sequence data of *Enterobacter cloacae* from NCBI

```
cttggcggca ggctaacac atgcaagtcg aacggtagca cagagagctt gctctgggtg gacgagtggc ggacgggtga gtaatgtctg ggaaactgcc tgatggaggg
ggataactac tggaaacggt agtaatacc gcataacgtc gcaagaccaa agagggggac cttcggcct cttgccatca gatgtgccca gatgggatta gctagtaggt
ggggtaacgg ctacacctagg cgacgatccc tagctggctt gagaggatga ccagccacac tggaaactgag acacgggtcca gactcctacg ggagggcagca gtgggggaata
ttgcacaatg ggcgcaagcc tgaatcagcc atgccgcgtg tatgaagaag gccctcgggt tgaagaatc tticagcggg gaggaagggtg ttgtgggtta taaccgcagc aattgacgtt
accgcagaa gaagcacccg ctaactcgt gccagcagcc gcggtaatac ggagggtgca agcgttaatc ggaattactg ggcgtaaagc gcacgcaggc ggtctgtcaa
gtcggatgtg aaatccccgg gctcaacctg ggaactgcat tcgaaactgg caggctagag tctigttagag gggggtagaa ttccagggt agcgggtgaaa tgcgtagaga
tctggaggaa tacgggtggc gaaggcgcc ccttggacaa agactgacct tcagggtcca aagcgtgggg agcaaacagg attagatacc ctggtagtcc acgcogtaaa
cgatgtcgac ttggagggtg tgccttgag gcgtggcttc cggagctaac gcgttaagtc gaccgcctgg ggagtagcgc cgcaaggta aaactcaaat gaattgacgg
ggggccgcac aagcggigga gcatgtggtt taatcgtatg caacggaag aaccttaact actcttgaca tccagagaac ttccagaga tggattggig ccttcgggaa ctctgagaca
ggigtgcat ggctgtctc agctcgtgtt gigaatgtt gggttaagtc ccgcaacagc cgcaacctt atccttgtt gccagcggc cggccgggaa ctcaaggag actgccagt
ataaacigga ggaagggtggg gatgacgica agtcatcatg gcccttacg gtagggctac acacgtgcta caatggcgca tacaagaga agcgaactcg cgagagcaag
cggacctcat aaagtgcgtc gtagtcgga ttggagictg caactgact ccatgaagtc ggaatcgta gtaatcgtag atcagaatgc tacgttccgg acgttccgg gccctgtaca
cacgccccgt cacacatgg gagtgggtg caaagaaggt aggtagctta acctcggga gggcgcttac cacttt
```

상기 검색된 *E. cloacae* 의 16S rRNA 유전자를 본원발명의 균주의 16S rRNA 와 비교한 결과는 다음과 같습니다.

scoring matrix: ,gap penalties: -12/-2

94.5% identity; Global alignment score: 5284

KCTC 0687BP : ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGGGCGGTAGCACAGGAGCTTGCT 60

[illegible]

E. cloacae : C-----CTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAGCACAGAGCCTTGCT 53

KCTC 0687BP : CCCGGGTGACGAGCGGCGGACGGGTGAGTAATGCTCTGGGAACTGCCCTGATGGAGGGGGA 120

[illegible]

E. cloacae : CTCGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTGGAACTGCCTGATGGAGGGGGA 113

KCTC 0687BP : TAACTACTGGAAACGGTAGCTAATACCGCATAACGTCTTCGGACCAAAGTGGGGGACCTT 180

[illegible]

E. cloacae : TAACTACTGGAAACGGTAGCTAATACCGCATAACGTGCAAGACCAAGAGGGGACCTT 173

KCTC 0687BP : CGGGCCTCATGCCATCAGATGTGCCAGATGGGATTAGCTAGTGGGTAAAGGCTC 240

[illegible]

E. cloacae : CGGGCCCTCTTGCCATCAGATGTGCCAGATGGGATTAGCTAGGTGGGTACGGCTC 233

KCTC 0687BP : ACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAAC TGAGACA 300

.....

E. cloacae : ACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACA 293

KCTC 0687BP : CGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGA 360

.....

E. cloacae : CGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAAATGGGCGCAAGCCTGA 353

KCTC 0687BP : TGCAGCCATGCCGCGTGTATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTCAGCGAGGAG 420

[illegible]

E. cloacae : TGCAGCCATGCCGCGTGTATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTACGCGGGGAG 413

KCTC 0687BP : GAAGGTGTTGTGGTTAATAACCACAGCAATTGACGTTACTCGCAGAGAAGCACCGGCTA 480

[illegible]

E. cloacae : GAAGGTGTTGTGGTTAATAACCGCAGCAATTGACGTTACCCGCAGAGAACCGGCTA 473

KCTC 0687BP : ACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGC 540

.....

E. cloacae : ACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGC 533

KCTC 0687BP : GTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCGGGCTCAACCTGGGA 600

.....

E. cloacae : GTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCGGCTCAACCTGGGA 593

KCTC 0687BP : ACTGCATTGGAACTGGCAAGCTTGAGTCTCGTAGAGGGGGTAGAATCCAGGTAGC 660

E. cloacae : ACTGCATTCCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAAATCCAGGTGTAGC 653

KCTC 0687BP : GGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGGCCCCCTGGACGAAGA 720

E. cloacae : GGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGCCCTTGGACAAAGA 713

KCTC 0687BP : CTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATTAGATACCCTGGTAGTCCACG 780

E. cloacae : CTGACCTTCAGGTGCCAAGCGTGGGGAGCAACAGGATTAGATACCCCTGGTAGTCCACG 773

KCTC 0687BP : CCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCG 840

E. cloacae : CCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCG 833

[illegible]

E. cloacae : TTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG 893

KCTC 0687BP : CCCGCACAAGCGGTGGAGCATGTGGTTTAA TTCGATGCAACGCCGAAGAACCTTACCTGGT 960

..... :
E. cloacae : CCCGCACAAGCGGTGGAGCATGTGGTTAATTCGATGCAACGCGAAGAACCCTTACCTACT 953

KCTC 0687BP : CTTGACATCCAGAGAATCCTGCAGAGATGCGGGAGTGCCTTCGGGAACCTCTGAGACACAGGT 1020
..... :
E. cloacae : CTTGACATCCAGAGAACTTCCAGAGATGGATTGGTGCCTTCGGGAACCTCTGAGACACAGGT 1013

KCTC 0687BP : GGTGATGGCTGTCGTCAGCTCGTGTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGC 1080
..... :
E. cloacae : GGTGATGGCTGTCGTCAGCTCGTGTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGC 1073

KCTC 0687BP : AACCTTATCCTTTGTTGCCAGCACGTAATGGTGGAACTCAAAGGAGACTGCCCGGTGAT 1140
..... :
E. cloacae : AACCTTATCCTTTGTTGCCAGCG-GTCCGGCCGGAACTCAAAGGAGACTGCCAGTGAT 1133

KCTC 0687BP : AAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACAC 1200
..... :
E. cloacae : AAACCTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACAC 1193

KCTC 0687BP : ACGTGCTACAATGGCGCATACAAAGAGAAAGCGACTCTCGGAGAGCAAGCGACCTCAT 1260

E. cloacae : ACGTGCTACAAATGGCGCATACAAAGAGAGCGAA-CTCGCGAGAGCAAGCGGACCTCATA 1253

KCTC 0687BP : AAGTGGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAG 1320

E. cloacae : AAGTGGGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAAATCGCTAG 1313

KCTC 0687BP : TAATCGTGGATCAGAAATGCCACGGTGAAATACGTTCCCGGGCCTTGATACACACGCCCGTC 1380

E. cloacae : TAATCGTAGATCAGAAATGCTACGGTGAATACGTTCCCGGGCCTTGACACACCGCCGTC 1373

KCTC 0687BP : ACACCATGGGAGTGGGTTGCCAAAAGAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACC 1440

E. cloacae : ACACCATGGGAGTGGGTGCAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACC 1433

KCTC 0687BP : ACTTTGTGATTCACTGGGGTG 1464

• •
• •
• •
• •
• •

E. cloacae : ACTTT-----1436



results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1051050953-025522-4328

Query=

(1449 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,729,678 sequences; 8,289,438,057 total letters

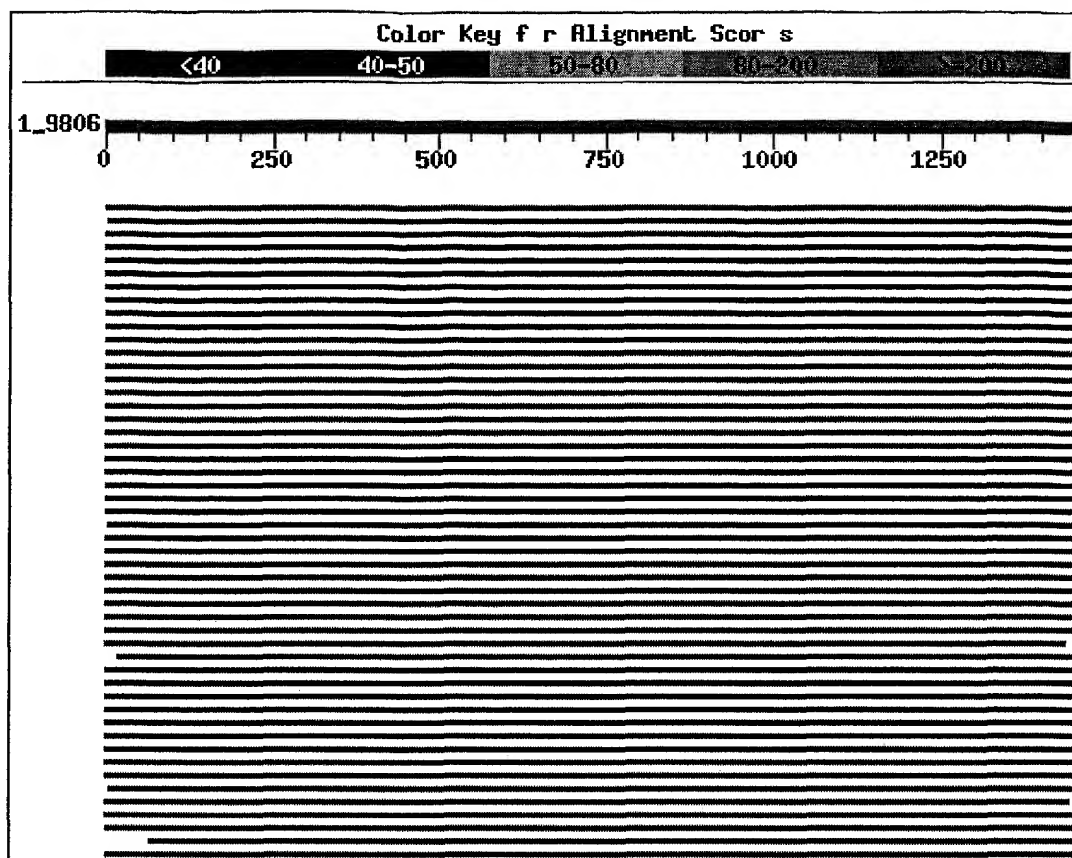
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

APPENDIX F



Sequences producing significant alignments:					Score (bits)	E Value
gi	2209038	dbj	AB004746.1	Enterobacter sakazakii gene for ...	2872	0.0
gi	3169776	gb	AF025366.1	AF025366 Citrobacter diversus stra...	2553	0.0
gi	16517821	gb	AF423229.1	Uncultured soil bacterium clone ...	2549	0.0
gi	1857865	gb	U88545.1	STU88545 Salmonella typhi 16S riboso...	2547	0.0
gi	2209047	dbj	AB004755.1	Klebsiella planticola gene for 1...	2535	0.0
gi	18644561	gb	AF371852.1	Uncultured bacterium clone p-217...	2522	0.0
gi	22758972	gb	AF534193.1	Uncultured bacterium clone Caf17...	2516	0.0
gi	29468966	gb	AY217654.1	Escherichia senegalensis 16S rib...	2492	0.0
gi	22758986	gb	AF534207.1	Uncultured bacterium clone Phe11...	2492	0.0
gi	1899234	gb	U90315.1	SMU90315 Salmonella matopeni Sml 16S...	2492	0.0
gi	1857864	gb	U88548.1	SPU88548 Salmonella paratyphi C 16S ...	2492	0.0
gi	3169774	gb	AF025364.1	AF025364 Citrobacter sedlakii 16S ...	2480	0.0
gi	2209040	dbj	AB004748.1	Enterobacter gergoviae gene for ...	2478	0.0
gi	3169780	gb	AF025370.1	AF025370 Citrobacter amalonaticus ...	2476	0.0
gi	6644288	gb	AF208013.1	AF208013 Enteric Group 137 16S rib...	2472	0.0
gi	3169773	gb	AF025363.1	AF025363 Citrobacter rodentium 16S...	2472	0.0
gi	4581981	emb	AJ233408.1	CFR233408 Citrobacter freundii 16...	2468	0.0
gi	1916302	gb	U92193.1	SBU92193 Salmonella bovis morbifican...	2468	0.0
gi	3169781	gb	AF025371.1	AF025371 Citrobacter farmeri 16S r...	2466	0.0
gi	3169775	gb	AF025365.1	AF025365 Citrobacter freundii 16S ...	2464	0.0
gi	20378116	gb	AF373198.1	Pantoea stewartii subsp. stewart...	2460	0.0
gi	4581997	emb	AJ233410.1	EAM233410 Erwinia amylovora 16S r...	2460	0.0
gi	3169779	gb	AF025369.1	Citrobacter sp. 'genomospecies 11...	2460	0.0
gi	13873050	gb	AF141895.1	AF141895 Erwinia amylovora strain...	2456	0.0

gi	3169783	gb	AF025373.1	AF025373	Citrobacter werkmanii 16S...	2454	0.0
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gi	2209050	dbj	AB004758.1		Pantoea ananas gene for 16S ribo...	2393	0.0
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gi 6714906 gb AF130981.1 AF130981	Klebsiella pneumoniae 16S...	2365	0.0

Alignments

Get selected sequences

Select all

Deselect all

>gi|2209038|dbj|AB004746.1| Enterobacter sakazakii gene for 16S ribosomal RNA, p
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Score = 2872 bits (1449), Expect = 0.0
Identities = 1449/1449 (100%)
Strand = Plus / Plus

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 Identities = 1405/1445 (97%)
 Strand = Plus / Plus

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Sbjct: 80 gacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataactac 139

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4/22/03

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4/22/03

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Identities = 1409/1449 (97%), Gaps = 1/1449 (0%)

Strand = Plus / Plus

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Sbjct: 572 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 631

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Query: 721 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 752 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 811

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 Sbjct: 1412 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1471

Query: 1441 gtgattcat 1449
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>gi|2209047|dbj|AB004755.1| Klebsiella planticola gene for 16S ribosomal RNA, pa
 Length = 1451

Score = 2535 bits (1279), Expect = 0.0
 Identities = 1406/1449 (97%)
 Strand = Plus / Plus

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Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacgaagactg 720
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Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
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 Sbjct: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449
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 Sbjct: 1441 gtgattcat 1449

>gi|18644561|gb|AF371852.1| Uncultured bacterium clone p-2172-s959-3 16S ribosom
 partial sequence
 Length = 1471

Score = 2522 bits (1272), Expect = 0.0
 Identities = 1406/1448 (97%), Gaps = 2/1448 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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 Sbjct: 26 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 83

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 84 gggtgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 143

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 144 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 203

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 264 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 323

Query: 301 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 504 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 563

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Sbjct: 564 aagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 623

Query: 601 gcatttgaaactgggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgggt 660
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Query: 781 taaacgatgtcgacttgagggttggtgcccttgaggcggtggcttcggagctaacgcgtta 840
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Sbjct: 804 taaacgatgtcgacttgagggttggtgcccttgaggcggtggcttcggagctaacgcgtta 863

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 864 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 923

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Sbjct: 924  gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 983

Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 984  gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1043

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Sbjct: 1044 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1103

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Sbjct: 1224 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1283

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Sbjct: 1404 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1463

Query: 1441 gtgattca 1448
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>gi|22758972|gb|AF534193.1| Uncultured bacterium clone Caf17 16S ribosomal RNA g
sequence
Length = 1462

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Identities = 1406/1449 (97%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

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Query: 61	tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa	120
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Sbjct: 244	taggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgg	303
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Sbjct: 1384 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1443

Query: 1441 gtgattcat 1449
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Sbjct: 1444 gtgattcat 1452

>gi|29468966|gb|AY217654.1| Escherichia senegalensis 16S ribosomal RNA gene, par
 Length = 1534

Score = 2492 bits (1257), Expect = 0.0
Identities = 1401/1449 (96%)
Strand = Plus / Plus

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 Sbjct: 1466 gtgattcat 1474

>gi|22758986|gb|AF534207.1| Uncultured bacterium clone Phe11 16S ribosomal RNA g
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 Length = 1462

Score = 2492 bits (1257), Expect = 0.0
 Identities = 1403/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

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 Sbjct: 6 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 63

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 124 ctactggaaacggtagctaataccgcataacgtcgcaagaccaaagagggggaccttcgg 183

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Sbjct: 484 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 543

Query: 541 aagcgcacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Query: 841 agtcgaccgcctggggagtagcggccgcaagggttaaaactcaaatgaattgacggggggccc 900
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Query: 961 gacatccagagaatcctgcagagatgcgggagtgacctcggaactctgagacaggtgct 1020
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Sbjct: 1144 tggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtagggctacacacgt 1203

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Sbjct: 1204 gctacaatggcgcatataaaagagaagcggaactcgcgagagcaagcggacctcataaagtg 1263

Query: 1261 cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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Sbjct: 1264 cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1323

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Sbjct: 1384 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1443

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Sbjct: 1444 gtgattcat 1452

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>gi|1899234|gb|U90315.1|SMU90315 Salmonella matopeni Sm1 16S ribosomal RNA gene,
Length = 1536

Score = 2492 bits (1257), Expect = 0.0
Identities = 1402/1449 (96%), Gaps = 6/1449 (0%)
Strand = Plus / Plus

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Query: 61      tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Sbjct: 92      gcctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 151

Query: 121     ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 152     ctactggaaacggta-----taccgcataacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181     gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240

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4/22/03

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Query: 61 tgctgacgagtggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Sbjct: 92 tgctgacgagtggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 151
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Sbjct: 152 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 211
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Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 212 gcctcttgccatcgatgtgccagatgggattagctagttggtgaggtaacggctcacc 271
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Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 272 aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgaagcacgg 331
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Sbjct: 332 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 391
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Query: 361 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
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Sbjct: 392 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 451
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Query: 421 ggtgttggtttaataaaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 452 ggtgttggtttaataaaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 511
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Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 512 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 571
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Query: 541 aagcgcacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 572 aagcgcacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 631
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Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 632 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 691
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Query: 661 gaaatgcgtagagatctggaggaataaccgggtggcggaaggcgccccctggacgaagactg 720
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Sbjct: 692 gaaatgcgtagagatctggaggaataaccgggtggcggaaggcgccccctggacgaagactg 751
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Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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4/22/03

Sbjct: 1472 gtgattcat 1480

>gi|3169774|gb|AF025364.1|AF025364 Citrobacter sedlakii 16S ribosomal RNA gene,
Length = 1522

Score = 2480 bits (1251), Expect = 0.0
Identities = 1399/1449 (96%)
Strand = Plus / Plus

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Sbjct: 507     ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541     aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct:	747	acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg	806
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Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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>gi|2209040|dbj|AB004748.1| Enterobacter gergoviae gene for 16S ribosomal RNA, p
 Length = 1450

Score = 2478 bits (1250), Expect = 0.0

Identities = 1399/1449 (96%)

Strand = Plus / Plus

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Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 121 ctactggaaacggtagctaataccgcataacgtcttcggaccaaagagggggaccttcgg 180

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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 Sbjct: 181 gcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaacggctcacc 240

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Query: 361 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
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 Sbjct: 1321 gtggatcagaatgccacggtgaataacgttcccgggccttgtagacacaccgcccgtcacacc 1380

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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 Sbjct: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449
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>gi|3169780|gb|AF025370.1|AF025370 Citrobacter amalonaticus 16S ribosomal RNA ge
 Length = 1525

Score = 2476 bits (1249), Expect = 0.0
 Identities = 1399/1449 (96%)
 Strand = Plus / Plus

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Query: 61 tgctgacgagtggtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Query: 421 ggtgttgtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 447 ggggttaagggttaataacccttagccattgacgttaccgcgagaagaagcaccggctaact 506

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Query: 541 aagcgcacgcagggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
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Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 987  gacatccacagaacttggcagagatgccttggtgccttcgggaactgtgagacaggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
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Sbjct: 1047 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
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Sbjct: 1167 tggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1407 atgggagtggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
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Sbjct: 1467 gtgattcat 1475

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>gi|6644288|gb|AF208013.1|AF208013 Enteric Group 137 16S ribosomal RNA gene, par
Length = 1538

Score = 2472 bits (1247), Expect = 0.0
Identities = 1396/1449 (96%)
Strand = Plus / Plus

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Query: 1  acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Sbjct: 29  acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctt 88

Query: 61  tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120

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Sbjct: 89  ygctgacgagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 148

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Sbjct: 149  ctactggaaacggtagctaataaccgcataaygtcgaagaccaaagagggggaccttcgg 208

Query: 181  gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 209  gcctcttgccatcggatgtgccagatgggattagcttggttggtgaggtaacggctcacc 268

Query: 241  taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Query: 421  ggtgttggtggttaataaccgcagcaattgacgttaccgcagaagaagcaccgggctaact 480
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Sbjct: 509  ccgtgccagcagccgcggttaataccggaggggtgcaagcggttaatcggaattactgggcgta 568

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Sbjct: 569  aagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 628

Query: 601  gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Query: 661  gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 720
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Sbjct: 689  gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 748

Query: 721  acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 749  acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 808

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Sbjct: 1049 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1108

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Sbjct: 1289 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1348

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Sbjct: 1409 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1468

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>gi|3169773|gb|AF025363.1|AF025363 *Citrobacter rodentium* 16S ribosomal RNA gene,
Length = 1496

Score = 2472 bits (1247), Expect = 0.0

Identities = 1398/1449 (96%)

Strand = Plus / Plus

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Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Sbjct: 86     cgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgggtggagggggataa 145

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 146    ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 205

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Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 266    aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 325

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Sbjct: 1406 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1465

Query: 1441 gtgattcat 1449
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Sbjct: 1466 gtgattcat 1474

>gi|4581981|emb|AJ233408.1|CFR233408 Citrobacter freundii 16S rRNA gene (strain
 Length = 1505

Score = 2468 bits (1245), Expect = 0.0
 Identities = 1398/1449 (96%)
 Strand = Plus / Plus

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Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 133 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 192

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Query: 1441 gtgattcat 1449
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>gi|1916302|gb|U92193.1|SBU92193 *Salmonella bovis* morbificans 16S ribosomal RNA
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 Length = 1541

Score = 2468 bits (1245), Expect = 0.0
 Identities = 1399/1449 (96%), Gaps = 1/1449 (0%)
 Strand = Plus / Plus

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 Sbjct: 1412 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1471

Query: 1441 gtgattcat 1449
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>gi|3169781|gb|AF025371.1|AF025371 *Citrobacter farmeri* 16S ribosomal RNA gene, p
 Length = 1511

Score = 2466 bits (1244), Expect = 0.0
 Identities = 1397/1449 (96%)
 Strand = Plus / Plus

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 Sbjct: 14 acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctc 73

Query: 61 tgctgacgagtggtggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 74 cgctgacgagtggtggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 133

Query: 121 ctactggaaacggtagctaataccgcataaacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 134 ctactggaaacggtagctaataccgcataaacgtcgcaagaccaaagagggggaccttcgg 193

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 794 taaacgatgtctatttgagggttggtgcccttgaggcgtggcttccggagctaacgcgtta 853

>[gi|3169775|gb|AF025365.1|AF025365](#) Citrobacter freundii 16S ribosomal RNA gene,
Length = 1523

Score = 2464 bits (1243), Expect = 0.0
Identities = 1397/1449 (96%)
Strand = Plus / Plus

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Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Sbjct: 327    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
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Sbjct: 387    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggaggaggaa 446

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>gi|20378116|gb|AF373198.1| Pantoea stewartii subsp. stewartii strain GSPB 2626
gene, partial sequence
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Identities = 1397/1449 (96%)
Strand = Plus / Plus

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Sbjct: 747 acgctcagggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 806

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcggtggttccggagctaacgcggtta 840
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Sbjct: 807 taaacgatgtcgacttggaggttgttcccttgaggagtggttccggagctaacgcggtta 866

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||
Sbjct: 867 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 926

Query: 901 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 927 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 986

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
|||||
Sbjct: 987 gacatccagcgaacttggcagagatgccttggtgccttcgggaacgctgagacaggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||
Sbjct: 1047 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||
Sbjct: 1107 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1166

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgt 1200
|||||
Sbjct: 1167 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtaggggtacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1227 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1286

Query: 1261 cgtcgtagtcggtgattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1287 cgtcgtagtcggtgattggagtcctgcaactcgactccgtgaagtcggaatcgctagtaatc 1346

Query: 1321 gtggatcagaatgccacggtgaataacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1347 gtggatcagaatgccacggtgaataacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1407 atgggagtggttgcaaaaagaagtaggtagcttaacccccgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
 ||||||||
 Sbjct: 1467 gtgattcat 1475

>gi|4581997|emb|AJ233410.1|EAM233410 Erwinia amylovora 16S rRNA gene (strain DSM
 Length = 1497

Score = 2460 bits (1241), Expect = 0.0
 Identities = 1399/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 13 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 70

Query: 61 tgctgacgagtggtgggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 71 ggtgacgagtggtgggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 130

Query: 121 ctactggaaacggtagcttaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 131 ctactggaaacggtagcttaataaccgcataacgtctacggaccaaagtgggggaccttcgg 190

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacgggtcacc 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 191 gcctcacaccatcggtatgtgccagatgggattagctggttaggtggggtaacgggtcacc 250

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 251 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 310

Query: 301 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

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|||||
Sbjct: 311 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 370

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 371 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 430

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||
Sbjct: 431 ggggaagagggttaataacctcctccattgacgttaccgcgagaagaagcaccggctaact 490

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcgttaatcggaattactgggcgta 540
|||||
Sbjct: 491 ccgtgccagcagccgcggttaatacggagggtgcaagcgttaatcggaattactgggcgta 550

Query: 541 aagcgcacgcaggcgggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 551 aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 610

Query: 601 gcatttgaaactggtcagcttgagtcctcgtagaggggggtagaattccagggtgtagcggt 660
|||||
Sbjct: 611 gcattcgaaactggcaggctagagtcctcgtagaggggggtagaattccagggtgtagcggt 670

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 671 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 730

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgccg 780
|||||
Sbjct: 731 acgctcaggtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgccg 790

Query: 781 taaacgatgtcgacttgagggttggtcccttgaggcgtggcttccggagctaacgcgtta 840
|||||
Sbjct: 791 taaacgatgtcgacttgagggttggtcccttgaggagtggttccggagctaacgcgtta 850

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||||
Sbjct: 851 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 910

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggctct 960
|||||
Sbjct: 911 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 970

Query: 961 gacatccagagaatcctgcagagatgcgggagtgacctcggaactctgagacagggtgct 1020
|||||
Sbjct: 971 gacatccacggaattctgcagagatgcggaagtgacctcggaaccgtgagacagggtgct 1030

Query: 1021 gcatggctgtcgtcagctcgtgtgtgaaatggtgggttaagtcccgcgaacgagcgcaac 1080
```



```

      |||
Sbjct: 1031 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcgcaacgagcgcaac 1090

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
      |||
Sbjct: 1091 ccttatcctttgttgccagcgattcggtcggggaactcaaaggagactgccggtgataaac 1150

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200
      |||
Sbjct: 1151 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1210

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
      |||
Sbjct: 1211 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1270

Query: 1261 cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
      |||
Sbjct: 1271 cgtcgtagtcgggattggagtcctgcaactcgactccgtgaagtcggaatcgctagtaatc 1330

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
      |||
Sbjct: 1331 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1390

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
      |||
Sbjct: 1391 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1450

Query: 1441 gtgattcat 1449
      |||
Sbjct: 1451 gtgattcat 1459

```

>gi|3169779|gb|AF025369.1| Citrobacter sp. 'genomospecies 11' 16S ribosomal RNA
sequence
Length = 1530

Score = 2460 bits (1241), Expect = 0.0
Identities = 1397/1449 (96%)
Strand = Plus / Plus

```

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
      |||
Sbjct: 27 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagaggagcttgctcctt 86

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
      |||
Sbjct: 87 gggtagcagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaaagtgggggaccttcgg 180

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Sbjct: 147 ||||| ctactggaaacggtagctaataaccgcataaacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
|||||

Sbjct: 207 gcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaacggctcacc 266

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||

Sbjct: 267 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||

Sbjct: 327 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361 agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaa 420
|||||

Sbjct: 387 agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggaggaggaa 446

Query: 421 ggtgttggtggttaataaaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||||

Sbjct: 447 ggtgttgagggttaataaacctcagcaattgacgttactcgcaagaagaagcaccggctaact 506

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
|||||

Sbjct: 507 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541 aagcgcacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||

Sbjct: 567 aagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 626

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
|||||

Sbjct: 627 gcacccgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcgg 686

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgggccccctggacgaagactg 720
|||||

Sbjct: 687 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgggccccctggacaaagactg 746

Query: 721 acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 747 acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 806

Query: 781 taaacgatgtcgacttgagggttggtcccttgaggcggttccggagctaacgcgtta 840
|||||

Sbjct: 807 taaacgatgtcgacttgagggttggtcccttgaggcggttccggagctaacgcgtta 866

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatgaattgacggggggccc 900

```

      |||
Sbjct: 867 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatgaattgacggggggccc 926

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
      |||
Sbjct: 927 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 986

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 987 gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
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Sbjct: 1047 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcgggtccggccgggaactcaaaggagactgccggtgataaac 1140
      |||
Sbjct: 1107 ccttatcctttgttgccagcgggtccggccgggaactcaaaggagactgccagtataaac 1166

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
      |||
Sbjct: 1167 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
      |||
Sbjct: 1227 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1286

Query: 1261 cgtcgtagtagcggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
      |||
Sbjct: 1287 tgtcgtagtagcggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1346

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1407 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
      |||
Sbjct: 1467 gtgattcat 1475

```

>gi|13873050|gb|AF141895.1|AF141895 Erwinia amylovora strain BC204 16S ribosomal
Length = 1480

Score = 2456 bits (1239), Expect = 0.0
Identities = 1398/1449 (96%), Gaps = 2/1449 (0%)

Strand = Plus / Plus

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Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
              |||
Sbjct: 3      acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 60

Query: 61      tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
              |
Sbjct: 61      gggtgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 120

Query: 121     ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
              |||
Sbjct: 121     ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180

Query: 181     gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
              |||
Sbjct: 181     gcctcacaccatcggatgtgcccagatgggattagctggttaggtgrggtaacggctcacc 240

Query: 241     taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
              |||
Sbjct: 241     taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

Query: 301     tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
              |||
Sbjct: 301     tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

Query: 361     agccatgccgcgtgtatgaagaaggccttcggggttgtaaagtactttcagcggggaggaa 420
              |||
Sbjct: 361     agccatgccgcgtgtatgaagaaggccttcggggttgtaaagtactttcagcggggaggaa 420

Query: 421     ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
              ||
Sbjct: 421     ggggaagaggttaataaccttttcattgacgttaccgcgagaagaagcaccggctaact 480

Query: 481     ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
              |||
Sbjct: 481     ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540

Query: 541     aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
              |||
Sbjct: 541     aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 600

Query: 601     gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
              |||
Sbjct: 601     gcattcgaaactggcaggctagagtctcgtagaggggggtagaattccaggtgtagcgg 660

Query: 661     gaaatgcgtagagatctggaggaataaccgggtggcgaggcgccccctggacgaagactg 720
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```

Sbjct: 661 gaaatgcgtagagatctggaggaataaccggtggcggaaggcgccccctggaogaagactg 720

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||

Sbjct: 781 taaacgatgtcgacttggaggttgtcccttgaggagtggcttccggagctaacgcgtta 840

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||

Sbjct: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900

Query: 901 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggctct 960
|||||

Sbjct: 901 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 960

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 961 gacatccacggaattctgcagagatgcggaagtgccttcgggaaccgtgagacaggtgct 1020

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
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Sbjct: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||

Sbjct: 1081 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1140

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200
|||||

Sbjct: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
|||||

Sbjct: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260

Query: 1261 cgtcgtagtccggattggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||

Sbjct: 1261 cgtcgtagtccggatcgaggtctgcaactcgactccgtgaagtcggaatcgctagtaatc 1320

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
||

Sbjct: 1321 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
|||||

Sbjct: 1381 atgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449

|||||||

Sbjct: 1441 gtgattcat 1449

>gi|3169783|gb|AF025373.1|AF025373 Citrobacter werkmanii 16S ribosomal RNA gene,
Length = 1521

Score = 2454 bits (1238), Expect = 0.0

Identities = 1393/1446 (96%)

Strand = Plus / Plus

Query: 4 ctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctctgc 63

Sbjct: 24 ctggcggcaggcctaacacatgcaagtcgaacggtagcacagagsagcttgctscttcgg 83

Query: 64 tgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataacta 123

Sbjct: 84 tgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataacta 143

Query: 124 ctggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcggggcc 183

Sbjct: 144 ctggaaacggtagctaataccgcataatgtcgaagaccaaagagggggaccttcggggcc 203

Query: 184 tcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacctag 243

Sbjct: 204 tcttgccatcggatgtgcccagatgggattagcttgttaggtggggtaacggctcacctag 263

Query: 244 gcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgggtcc 303

Sbjct: 264 gcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgggtcc 323

Query: 304 agactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagc 363

Sbjct: 324 agactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagc 383

Query: 364 catgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaaggt 423

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Sbjct: 444 gttgtggttaataaccacagcaattgacgttactcgcagaagaagcaccgggctaactccg 503

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Sbjct: 504 tgccagcagccgcggtaataacggaggggtgcaagcggttaatcggaattactgggcgtaaag 563

4/22/03

Query: 1264 cgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcgtg 1323
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 Sbjct: 1284 cgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcgtg 1343

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Query: 1444 attcat 1449
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>gi|13873049|gb|AF141894.1|AF141894 Erwinia amylovora strain BC203 16S ribosomal
 Length = 1480

Score = 2452 bits (1237), Expect = 0.0
 Identities = 1397/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

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 Sbjct: 61 gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 120

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180

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 Sbjct: 181 gcctcacaccatcgatgtgcccagatgggattagctggttaggtggggtaacggctcacc 240

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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 Sbjct: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

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Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 421 gggkragagggttaataacctyctgcattgacgttaccgcgagaagaagcaccggctaact 480

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540

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Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 661 gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 720

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Sbjct: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 900

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 |||
 Sbjct: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260

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 Sbjct: 1261 cgctcgtagtcggtgattggagtcgtgcaactcgactccatgaagtcggaatcgctagtaatc 1320

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 Sbjct: 1321 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380

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 |||
 Sbjct: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449
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>gi|11907474|emb|AJ277977.1|LAD277977 Leclercia adecarboxylata 16S rRNA gene, st
 Length = 1447

Score = 2452 bits (1237), Expect = 0.0
 Identities = 1399/1448 (96%), Gaps = 5/1448 (0%)
 Strand = Plus / Plus

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 Sbjct: 1 cgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctcg 58

Query: 62 gctgacgagtggtggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 121
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 Sbjct: 59 ggtgacgagtggtggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 118

Query: 122 tactggaaacggtagctaataaccgcataacgtctacggaccaaagtggggggaccttcggg 181
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 Sbjct: 119 tactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcggg 178

Query: 182 cctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacct 241
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Sbjct: 179 cctcttgccatcagatgtgccagatgggattagctagtaggtggggtaatggctcacct 238

Query: 242 aggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacggt 301
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Sbjct: 239 aggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacggt 298

Query: 302 ccagactcctacgggaggcagcagtggggaatattgcacaatggcgcaagcctgatgca 361
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Sbjct: 299 ccagactcctacgggaggcagcagtggggaatattgcacaatggcgcaagcctgatgca 358

Query: 362 gccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaag 421
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Sbjct: 359 gccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaag 418

Query: 422 gtgttggtggttaataaccgcagcaattgacgttaccgcagaagaagcaccggctaactc 481
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Query: 482 cgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgtaa 541
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Query: 602 catttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggtg 661
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Sbjct: 899  cacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactcttg 958

Query: 962  acatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgctg 1021
          ||||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 959  acatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgctg 1018

Query: 1022 catggctgtcgtcagctcgtgttgtaaagtgttggttaagtcgccgcaacgagcgcaacc 1081
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Sbjct: 1019 catggctgtcgtcagctcgtgttgtaaagtgttggttaagtcgccgcaacgagcgcaacc 1078

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Query: 1142 ggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgtg 1201
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Query: 1262 gtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcg 1321
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Sbjct: 1259 gtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcg 1318

Query: 1322 tggatcagaatgccacgggtgaatacgttcccgggccttgtaacacaccgcccgtcacacca 1381
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Sbjct: 1319 tagatcagaatgctacgggtgaatacgttcccgggccttgtaacacaccgcccgtcacacca 1378

Query: 1382 tgggagtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttg 1441
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Sbjct: 1379 tgggagtggggttgcaaaagaagtaggtagcttaaccttcgg--aggcgc-taccactttg 1435

Query: 1442 tgattcat 1449
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>gi|3169778|gb|AF025368.1|AF025368 Citrobacter braakii 16S ribosomal RNA gene, p
Length = 1530

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Identities = 1396/1449 (96%)
Strand = Plus / Plus

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Sbjct: 87  gggtgacgagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 147 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 267 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

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Sbjct: 327 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

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Sbjct: 507 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 687 gaaatgcgtagagatctggaggaataaccggtggcgaaaggcgccccctggacaaagactg 746

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Sbjct: 1107 ccttatcctttgttgccagcgggtccggccgggaactcaaaggagactgccagtgataaac 1166

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Sbjct: 1407 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
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Sbjct: 1467 gtgattcat 1475

>gi|4581973|emb|AJ233403.1|BGA233403 Buttiauxella gaviniae 16S rRNA gene (strain
Length = 1495

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Identities = 1398/1451 (96%), Gaps = 6/1451 (0%)
Strand = Plus / Plus

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|||||||
Sbjct: 10 acgctggcggcaggcctaacaacatgcaagtcgagcggtagcacagggagcttgctcctg- 68

Query: 59 tctgctgacgagtgggcggacgggtgagtaatgtctgggaaactgcctgatggagggggat 118
| |||||
Sbjct: 69 ---ggtgacgagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggat 125

Query: 119 aactactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttc 178
|||||||
Sbjct: 126 aactactggaaacggtagctaataaccgcataacgtcttcggaccaaagagggggaccttc 185

Query: 179 gggcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctca 238
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Sbjct: 186 gggcctcctgccatcagatgtgccagatgggattagctagtaggtgaggtaatggctca 245

Query: 239 cctaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacac 298
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Query: 299 ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat 358
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Query: 359 gcagccatgccgctgtatgaagaaggccttcggggtgtaaagtactttcagcggggagg 418
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Query: 419 aagggtgttggtgtaataaccgcagcaattgacgttaccgcagaagaagcaccgggctaa 478
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Query: 599 ctgcatttgaaactgggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcg 658
||||| ||||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Sbjct: 606 ctgcattcgaaactggcaagctagagtctttagaggggggtagaattccaggtgtagcg 665

Query: 659 gtgaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagac 718
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Sbjct: 666 gtgaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacaaagac 725

Query: 719 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc 778
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Sbjct: 726 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc 785

Query: 779 cgtaaacgatgtcgacttgagggttggtgcccttgaggcggtggcttccggagctaacgcgt 838
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Sbjct: 786 cgtaaacgatgtcgacttgagggttggtgcccttgaggagtggttccggagctaacgcgt 845

Query: 839 taagtcgaccgcctggggagtagcgccgcaagggttaaaactcaaattgaattgacgggggc 898
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Sbjct: 846 taagtcgaccgcctggggagtagcgccgcaagggttaaaactcaaattgaattgacgggggc 905

Query: 899 ccgcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtc 958
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Sbjct: 906 ccgcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactc 965

Query: 959 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
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Sbjct: 966 ttgacatccacagaattcggcagagatgccttagtgcccttcgggaactgtgagacaggtg 1025

Query: 1019 ctgcatggctgtcgtcagctcgtgttgtaaattgttgggttaagtcctcgcaacgagcgca 1078
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Sbjct: 1026 ctgcatggctgtcgtcagctcgtgttgtaaattgttgggttaagtcctcgcaacgagcgca 1085

Query: 1079 acccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataa 1138
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Sbjct: 1086 acccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccagtataa 1145

Query: 1139 accggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacac 1198
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Sbjct: 1146 actggaggaaggtggggatgacgtcaagtcacatggcccttacgagtagggctacacac 1205

Query: 1199 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1258
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Sbjct: 1206 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1265

Query: 1259 tgcgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaa 1318
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Sbjct: 1266 tgcgtcgtagtcggtacggtacggtctgcaactcgactccgtgaagtcggaatcgctagtaa 1325

Query: 1319 tcgtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1378

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Sbjct: 1326 tcgtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1385

Query: 1379 ccatgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1438

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Sbjct: 1386 ccatgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1445

Query: 1439 ttgtgattcat 1449

|||||
Sbjct: 1446 ttgtgattcat 1456

>gi|14549203|dbj|AB053117.1| Klebsiella oxytoca gene for 16S rRNA
Length = 1492

Score = 2448 bits (1235), Expect = 0.0
Identities = 1397/1449 (96%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggagcagcttgctgctc 60
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Sbjct: 25 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 82

Query: 61 tgctgacgagtggtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
|
Sbjct: 83 ggggtgacgagtggtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 142

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 143 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 202

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
|||||
Sbjct: 203 gcctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 262

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 263 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 322

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 323 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 382

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 383 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 442

4/22/03

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgt 1200
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 Sbjct: 1163 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtagggctacacacgt 1222

Query: 1201 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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 Sbjct: 1223 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1282

Query: 1261 cgtcgtagtagccggttgaggatctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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 Sbjct: 1283 tgtcgtagtagccggttgaggatctgcaactcgactccatgaagtcggaatcgctagtaatc 1342

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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 Sbjct: 1343 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1402

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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 Sbjct: 1403 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1462

Query: 1441 gtgattcat 1449
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 Sbjct: 1463 gtgattcat 1471

>gi|11907475|emb|AJ277978.1|LAD277978 Leclercia adecarboxylata 16S rRNA gene, st
 Length = 1437

Score = 2444 bits (1233), Expect = 0.0
 Identities = 1390/1437 (96%), Gaps = 4/1437 (0%)
 Strand = Plus / Plus

Query: 2 cgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctct 61
 |||||||||||||||||||||||||||||||||||||||| || |||
 Sbjct: 1 cgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctcg 58

Query: 62 gctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 121
 | ||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 59 ggtgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 118

Query: 122 tactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcggg 181
 ||||||||||| ||||||||||||||||||||||||||||||||||||||
 Sbjct: 119 tactggaaacggtagctaataccgcataacgtcgcaagaccaaagagggggaccttcggg 178

Query: 182 cctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacct 241
 ||||| ||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 179 cctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacct 238

Query: 242 aggcgacgatccctagct-ggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 239 aggcgacgatccctagcttggctgagaggatgaccagccacactggaactgagacacgg 298

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 299 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 358

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 359 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 418

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||||
Sbjct: 419 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 478

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 479 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 538

Query: 541 aagcgcacgcaggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 539 aagcgcacgcaggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 598

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 599 gcattcgaaactggcaggctagagtctttagaggggggtagaattccaggtgtagcgg 658

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 659 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacaaagactg 718

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 719 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 778

Query: 781 taaacgatgtcgacttggaggttggtcccttgaggcggtggttccggagctaacgcgtta 840
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Sbjct: 779 taaacgatgtcgacttggaggttggtcccttgaggagtggttccggagctaacgcgtta 838

Query: 841 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaatagaattgacggggggccc 900
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Sbjct: 839 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaatagaattgacggggggccc 898

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtcctt 960
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Sbjct: 899 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactcctt 958

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Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 959  gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1018

Query: 1021  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
          |||
Sbjct: 1019  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1078

Query: 1081  ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Sbjct: 1079  ccttatcctttgttgccagcgggttaggccgggaactcaaaggagactgccagtataaac 1138

Query: 1141  cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
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Sbjct: 1139  tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1198

Query: 1201  gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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Sbjct: 1199  gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1258

Query: 1261  cgtcgtagtcaggattggagctctgcaactcgactccatgaa-gtcggaatcgctagtaat 1319
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Sbjct: 1259  cgtcgtagtcaggattggagctctgcaactcgactccatgaagggtcggaatcgctagtaat 1318

Query: 1320  cgtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacac 1379
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Sbjct: 1319  cgtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacac 1378

Query: 1380  catgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttacca 1436
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Sbjct: 1379  catgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttacca 1435

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>gi|2584810|emb|Z96080.1|PSZ96080 Pantoea stewartii LMG 2715 16S ribosomal RNA
Length = 1497

Score = 2444 bits (1233), Expect = 0.0
Identities = 1393/1449 (96%)
Strand = Plus / Plus

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Query: 1  acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Sbjct: 6  acgctggcggcaggcctaacacatgcaagtcggacggtagcacagaggagcttgctcctc 65

Query: 61  tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
          |
Sbjct: 66  gggtagcagagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 125

```

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 126 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagtgggggacctccgg 185

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 186 gcctcacaccatcggtatgtgcccagatgggattagctagtaggcgggtaacggcccacc 245

Query: 241 taggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 246 taggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgg 305

Query: 301 tccagactcctacgggaggcagcagtggggaatatgtcaccaatgggcgcaagcctgatgc 360
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Sbjct: 306 tccagactcctacgggaggcagcagtggggaatatgtcaccaatgggcgcaagcctgatgc 365

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 366 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcgggrraggaa 425

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 426 ggtggtgaggttaataacctcatcaattgacgttaccgcgagaaraagcaccggctaact 485

Query: 481 ccgtgccagcagccgcggtataacggagggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 486 ccgtgccagcagccgcggtataacggagggtgcaagcggttaatcggaattactgggcgta 545

Query: 541 aagcgcacgcagcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 606 gcatttgaaactggcaggcttgagtctcgtagaggggggtagaattccaggtgtagcgg 665

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 666 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 725

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 726 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 785

Query: 781 taaacgatgtcgacttgagggttggtcccttgaggcgtggcttcggagctaacgcgtta 840
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Sbjct: 786 taaacgatgtcgacttgagggttggtcccttgaggagtggcttcggagctaacgcgtta 845

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Query: 841  agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
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Sbjct: 846  agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 905

Query: 901  gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 960
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Sbjct: 906  gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 965

Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 966  gacatccagcgaacttggcagagatgccttggtgccttcgggaacgctgagacaggtgct 1025

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgttgggttaagtcccgcaacgagcgcaac 1080
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Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Sbjct: 1086 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1145

Query: 1141 cggaggaaggtggggatgacgtcaagtcatcatggcccttacgaccagggtacacacgt 1200
          ||||||||| ||| ||||||||| ||||||||||||| |||||||||||||
Sbjct: 1146 cggaggaaggtggggatgacgtcaagtcatcatggcccttacgagtaggggtacacacgt 1205

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
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Sbjct: 1206 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaastg 1265

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
          ||||||||| ||| ||||||||| ||||||||||||| |||||||||||||
Sbjct: 1266 cgtcgtagtccggatcgagctctgcaactcgactccgtgaagtcggaatcgctagtaatc 1325

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
          ||||||||| ||| ||||||||| ||||||||||||| |||||||||||||
Sbjct: 1326 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1385

Query: 1381 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1386 atgggagtggttgcaaaagaagtaggttagcttaacccccgggagggcgcttaccacttt 1445

Query: 1441 gtgattcat 1449
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Sbjct: 1446 gtgattcat 1454

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>gi|3218459|emb|X83265.1|EA16SRR E.amylovora 16S rRNA gene
Length = 1502

Score = 2444 bits (1233), Expect = 0.0

Identities = 1398/1449 (96%), Gaps = 3/1449 (0%)
Strand = Plus / Plus

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Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Sbjct: 26     acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 83

Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
             |
Sbjct: 84     gggtgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 143

Query: 121    ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
             |||||||
Sbjct: 144    ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 203

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 204    gcctcacaccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 263

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
             |||||||
Sbjct: 264    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 323

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 324    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 383

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaa 420
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Sbjct: 384    agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaa 443

Query: 421    ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 444    ggggaagaggttaataaccttttccattgacgttaccgcgagaagaagcaccggctaact 503

Query: 481    ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
             |||||||
Sbjct: 504    ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta 563

Query: 541    aagcgcacgcaggcgggtgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
             |||||||
Sbjct: 564    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 623

Query: 601    gcatttgaaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggg 660
             |||||||
Sbjct: 624    gcattcgaaaactggcaggctagagtctcgtagaggggggtagaattccaggtgtagcggg 683

Query: 661    gaaatgcgtagagatctggaggaataaccgggtggcgaggcgccccctggacgaagactg 720
```


Sbjct: 684 ||||| gaaatgcgtagagatctggaggaataaccggtggcggaaggcgccccctggacgaagactg 743

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 744 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 803

Query: 781 taaacgatgtcgacttggagggtgtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||

Sbjct: 804 taaacgatgtcgacttggagggtgttcccctgaggagtggcttccggagctaacgcgtta 863

Query: 841 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaattgaattgacggggggccc 900
|||||

Sbjct: 864 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaattgaattgacggggggccc 923

Query: 901 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtcct 960
|||||

Sbjct: 924 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 983

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacagggtgct 1020
|||||

Sbjct: 984 gacatccacggaattctgcagagatgcggaagtgcccttcgggaacctgagacagggtgct 1043

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||

Sbjct: 1044 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1103

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||

Sbjct: 1104 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1163

Query: 1141 cggaggaaggtggggatgacgtcaagtcattcatggcccttacgaccagggtacacacgt 1200
|||||

Sbjct: 1164 cggaggaaggtggggatgacgtcaagtcattcatggcccttacgaccagggtacacacgt 1223

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
|||||

Sbjct: 1224 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1283

Query: 1261 cgtcgtagtccggattggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||

Sbjct: 1284 cgtcgtagtccggatcggagtctgcaactcgactccgtgaagtcggaatcgctagtaatc 1343

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||||

Sbjct: 1344 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1403

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

|||||
 Sbjct: 1404 atgggagtggttgcaaaagaagtaggtagcttaa-cttcgggagggcgcttaccacttt 1462

Query: 1441 gtgattcat 1449

|||||
 Sbjct: 1463 gtgattcat 1471

>gi|4753688|emb|AJ010485.1|EAM010485 Erwinia amylovora 16S rRNA gene, tRNA-Glu g
 gene
 Length = 2016

Score = 2444 bits (1233), Expect = 0.0
 Identities = 1398/1449 (96%), Gaps = 3/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 26 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 83

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |
 Sbjct: 84 gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 143

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||||
 Sbjct: 144 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 203

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
 |||||
 Sbjct: 204 gcctcacaccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 263

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
 |||||
 Sbjct: 264 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 323

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
 |||||
 Sbjct: 324 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 383

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
 |||||
 Sbjct: 384 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 443

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
 ||
 Sbjct: 444 ggggaagaggttaataaccttttccattgacgttaccgcgagaagaagcaccgggctaact 503

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540

Sbjct: 504 |||||ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 563

Query: 541 aagcgcacgcagcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||

Sbjct: 564 aagcgcacgcagcggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 623

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 660
|||||

Sbjct: 624 gcattcgaaactggcaggctagagtctcgtagaggggggtagaattccaggtgtagcggt 683

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 720
|||||

Sbjct: 684 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 743

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 744 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 803

Query: 781 taaacgatgtcgacttgagggtgtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||

Sbjct: 804 taaacgatgtcgacttgagggtgttcccctgaggagtggcttccggagctaacgcgtta 863

Query: 841 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||

Sbjct: 864 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaatagaattgacggggggccc 923

Query: 901 gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 960
|||||

Sbjct: 924 gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 983

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
|||||

Sbjct: 984 gacatccacggaattctgcagagatgcggaagtgcccttcgggaacctgagacaggtgct 1043

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtggtgggtaagtcccgcaacgagcgcaac 1080
|||||

Sbjct: 1044 gcatggctgtcgtcagctcgtgttgtaaagtggtgggtaagtcccgcaacgagcgcaac 1103

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||

Sbjct: 1104 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1163

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
|||||

Sbjct: 1164 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1223

Query: 1201 gctacaatggcgcatacaaagagaagcgacctcgcgagagcaagcggaacctcataaagtg 1260

```

|||||
Sbjct: 1224 gctacaatggcgcatatacaagagaagcgacctcgcgagagcaagcggaacctcataaagtg 1283

Query: 1261 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||
Sbjct: 1284 cgtcgtagtcgggatcgagctctgcaactcgactccgtgaagtcggaatcgctagtaatc 1343

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||
Sbjct: 1344 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1403

Query: 1381 atgggagtggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
|||||
Sbjct: 1404 atgggagtggggtgcaaaagaagtaggtagcttaa-cttcgggagggcgcttaccacttt 1462

Query: 1441 gtgattcat 1449
|||||
Sbjct: 1463 gtgattcat 1471

```

>gi|22947742|gb|AY133084.1| Uncultured gamma proteobacterium clone ccs1m2118 16S
 gene, partial sequence
 Length = 1450

Score = 2440 bits (1231), Expect = 0.0
 Identities = 1381/1430 (96%), Gaps = 1/1430 (0%)
 Strand = Plus / Plus

```

Query: 19  acacatgcaagtcgaacggtaacagggagcagcttgctgctctgctgacgagtgggcgac 78
|||||
Sbjct: 15  acacatgcaagtcgaacggtaacaggaagcagcttgctgctttgctgacgagtgggcgac 74

Query: 79  ggggtgagtaatgtctgggaaactgcctgatggaggggggataactactggaaacggtagct 138
|||||
Sbjct: 75  ggggtgagtaatgtctgggaaactgcctggtggaggggggataactactggaaacggtagct 134

Query: 139  aataccgcataacgtctacggaccaaagtgggggaccttcgggcctcatgccatcagatg 198
|||||
Sbjct: 135  aataccgcataacgtcgcaagaccaaagaggggggaccttcgggcctcttgccatcggatg 194

Query: 199  tgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgacgatccctagc 258
|||||
Sbjct: 195  tgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgacgatccctagc 254

Query: 259  tggctctgagaggatgaccagccacactggaactgagacacgggtccagactcctacgggag 318
|||||
Sbjct: 255  tggctctgagaggatgaccagccacactggaactgagacacgggtccagactcctacgggag 314

Query: 319  gcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccatgccgcgtgtatg 378

```

Sbjct: 315 |||gcagcagtgagggaatatgacacaatgggcgcaagcctgatgcagccatgccgcgtgatg 374

Query: 379 aagaaggccttcgggttgtaaagtactttcagcggggaggaagggtgttggttaataac 438
|||

Sbjct: 375 aagaaggccttcgggttgtaaagtactttcagcggggaggaaggcgataagggttaataac 434
|||

Query: 439 cgcagcaattgacgttacccgcagaagaagcaccggctaactccgtgccagcagccgcgg 498
|

Sbjct: 435 cttgtcgattgacgttacccgcagaagaagcaccggctaactccgtgccagcagccgcgg 494
|

Query: 499 taatacggagggtgcaagcgtaatacggaattactgggcgtaaagcgcacgcaggcggtt 558
|||

Sbjct: 495 taatacggagggtgcaagcgtaatacggaattactgggcgtaaagcgcacgcaggcggtc 554
|||

Query: 559 gattaagtcagatgtgaaatccccgggctcaacctgggaactgcatttgaaactggtcag 618
|

Sbjct: 555 tgtcaagtcggatgtgaaatccccgggctcaacctgggaactgcattcgaaactggcagg 614
|

Query: 619 cttgagtctcgtagagggggtagaattccaggtgtagcggtgaaatgcgtagagatctg 678
||

Sbjct: 615 ctagagtctttagagggggtagaattccaggtgtagcggtgaaatgcgtagagatctg 674
||

Query: 679 gaggaataccggtggcgaaggcgccccctggacgaagactgacgctcaggtgcgaaagc 738
|||

Sbjct: 675 gaggaataccggtggcgaaggcgccccctggacaaagactgacgctcaggtgcgaaagc 734
|||

Query: 739 gtggggagcaaacaggattagataaccctggtagtccacgccgtaaacgatgtcgacttgg 798
|||

Sbjct: 735 gtggggagcaaacaggattagataaccctggtagtccacgccgtaaacgatgtcgacttgg 794
|||

Query: 799 aggttggtgcccttgaggcgtggcttccggagctaacgcgttaagtcgaccgcctggggag 858
|||

Sbjct: 795 aggttggtgcccttgaggcgtggcttccggagctaacgcgttaagtcgaccgcctggggag 854
|||

Query: 859 tacggccgcaaggttaaaactcaaatgaattgacggggggcccgacaaagcgggtggagcat 918
|||

Sbjct: 855 tacggccgcaaggttaaaactcaaatgaattgacggggggcccgacaaagcgggtggagcat 914
|||

Query: 919 gtggtttaattcgatgcaacgcgaagaaccttacctgggtcttgacatccagagaatcctg 978
|||

Sbjct: 915 gtggtttaattcgatgcaacgcgaagaaccttacctactcttgacatccagagaacttag 974
|||

Query: 979 cagagatgcgggagtgcccttcgggaactctgagacagggtgctgcatggctgtcgtcagct 1038
|||

Sbjct: 975 cagagatgcttgggtgccttcgggaactctgagacagggtgctgcatggctgtcgtcagct 1034
|||

Query: 1039 cgtgttggtgaaatgttgggttaagtcccgcaacgagcgcaacccttatccttggttgcca 1098

```

      |||
Sbjct: 1035 cgtgttggtgaaatggtgggttaagtcccgcaacgagcgcaacccatatacctttgttgcca 1094

Query: 1099 gcggttcggccgggaactcaaaggagactgccggtgataaaccggaggaagggtggggatg 1158
      |||
Sbjct: 1095 gcggttaggccgggaactcaaaggagactgccagtataaactggaggaagggtggggatg 1154

Query: 1159 acgtcaagtcacatcatggcccttacgaccagggtacacacgtgctacaatggcgcataca 1218
      |||
Sbjct: 1155 acgtcaagtcacatcatggcccttacgagtaggggtacacacgtgctacaatggcgcataca 1214

Query: 1219 aagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtcgtagtccggattgg 1278
      |||
Sbjct: 1215 aagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtcgtagtccggattgg 1274

Query: 1279 agtctgcaactcgactccatgaagtgcgaatcgctagtaatcgtaggattcagaatgccacg 1338
      |||
Sbjct: 1275 agtctgcaactcgactccatgaagtgcgaatcgctagtaatcgtaggattcagaatgccacg 1334

Query: 1339 gtgaatacgttcccgggccttgtagacacaccgcccgtcacaccatgggagtggggttgcaaa 1398
      |||
Sbjct: 1335 gtgaatacgttcccgggccttgtagacacaccgcccgtcacaccatgggagtggggttgcaaa 1394

Query: 1399 agaagtaggtagcttaaccttcgggagggcgcttaccactttgtgattca 1448
      |||
Sbjct: 1395 agaagtaggtagcttaaccttcgggagggcgcttaccac-ttgtagattca 1443

```

>gi|4582061|emb|AJ233414.1|EMA233414 Erwinia mallotivora 16S rRNA gene (strain D)
Length = 1504

Score = 2436 bits (1229), Expect = 0.0
Identities = 1394/1449 (96%)
Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
      |||
Sbjct: 14     acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagggagcttgctcct 73

Query: 61     tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
      |||
Sbjct: 74     gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 133

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
      |||
Sbjct: 134    ctactggaaacggtagctaataaccgcataacgtcttcggaccaaagtgggggaccttcgg 193

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
      |||

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4/22/03

```

Sbjct: 914  gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 973

Query: 961  gacatccagagaatcctgcagagatgcgggagtgcttcgggaactctgagacaggtgct 1020
          |||||  |||  |||||  ||  |||||  ||  |||||  |||||  |||||  |||||
Sbjct: 974  gacatccacggaagacctcagagatggggttgctgccttcgggaaccgtgagacaggtgct 1033

Query: 1021  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcgcgcaacgagcgcaac 1080
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1034  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcgcgcaacgagcgcaac 1093

Query: 1081  ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
          |||||  |||||  |||||  ||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1094  ccttatcctttgttgccatcgattcggtcgggaactcaaaggagactgccggtgataaac 1153

Query: 1141  cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccaggggtacacacgt 1200
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1154  cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccaggggtacacacgt 1213

Query: 1201  gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1214  gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1273

Query: 1261  cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1274  cgtcgtagtcgggattggagtcctgcaactcgactccgtgaagtcggaatcgctagtaatc 1333

Query: 1321  gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1334  gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1393

Query: 1381  atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 1394  atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1453

Query: 1441  gtgattcat 1449
          |||||
Sbjct: 1454  gtgattcat 1462

```

>gi|3282039|emb|Y17667.1|KOY17667 Klebsiella oxytoca 16S rRNA gene, strain i128-
Length = 1452

Score = 2434 bits (1228), Expect = 0.0
Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

```

Query: 1  acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 4  acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 61

```


4/22/03

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcggtggcttccggagctaacgcgtta 840
|||||
Sbjct: 782 taaacgatgtcgacttggaggttgttcccttgaggagtggttccggagctaacgcgtta 841

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||||
Sbjct: 842 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 901

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 902 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 961

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcttccgggaactctgagacaggtgct 1020
|||||
Sbjct: 962 gacatccagagaacttagcagagatgcttgggtgccttccgggaactctgagacaggtgct 1021

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||
Sbjct: 1022 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1081

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||
Sbjct: 1082 ccttatcctttgttgccagcgattcggycgggaactcaaaggagactgccagtgataaac 1141

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
|||||
Sbjct: 1142 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1201

Query: 1201 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
|||||
Sbjct: 1202 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||
Sbjct: 1262 tgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||||
Sbjct: 1322 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1381

Query: 1381 atgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
|||||
Sbjct: 1382 atgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441 gtgattcat 1449
|||||
Sbjct: 1442 gtgattcat 1450

>gi|2584741|emb|Z96078.1|ECZ96078 Enterobacter cancerogenus LMG 2693 16S ribosom
Length = 1495

Score = 2432 bits (1227), Expect = 0.0
Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

```
Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
             |||
Sbjct: 6      acgctggcggcaggcctaacacatgcaagtcgarccgtarccacagag-agcttgct-ctc 63

Query: 61     tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
             |||
Sbjct: 64     gggtgacgagyggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 123

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
             |||
Sbjct: 124    ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 183

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
             |||
Sbjct: 184    gcctcctgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 243

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
             |||
Sbjct: 244    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 303

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
             |||
Sbjct: 304    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaascctgatgc 363

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
             |||
Sbjct: 364    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 423

Query: 421    ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
             |||
Sbjct: 424    ggcgataagggttaataaccttgcgattgacgttaccgcgagaaraagcaccgggctaact 483

Query: 481    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
             |||
Sbjct: 484    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 543

Query: 541    aagcgcacgcaggcgggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
             |||
Sbjct: 544    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 603
```

4/22/03

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 || |||||
 Sbjct: 1324 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1383

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 1384 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1443

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 1444 gtgattcat 1452

>gi|1359900|emb|X93216.1|KP16SRRN2 K.planticola 16S rRNA gene (strain DR3)
 Length = 1495

Score = 2432 bits (1227), Expect = 0.0
 Identities = 1394/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 6 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagag-agcttgct-ctc 63

Query: 61 tgctgacgagtggtggcggacgggtgagtaatgtctgggaaactgcctgatggaggggggataa 120
 |||||
 Sbjct: 64 ggttgacgagcggcggacgggtgagtaatgtctgggaaactgcctgatggaggggggataa 123

Query: 121 ctactggaaacggtagcttaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||||
 Sbjct: 124 ctactggaaacggtagcttaataaccgcataacgtcgcaagaccaaagtgggggaccttcgg 183

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
 |||||
 Sbjct: 184 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaaatggctcacc 243

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
 |||||
 Sbjct: 244 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 303

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
 |||||
 Sbjct: 304 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 363

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
 |||||
 Sbjct: 364 agccatcccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggaggaggaa 423

4/22/03

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200
 |||||
 Sbjct: 1144 tggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtagggctacacacgt 1203

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
 |||||
 Sbjct: 1204 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1263

Query: 1261 cgtcgtagtcggttgaggctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||||
 Sbjct: 1264 tgtcgtagtcggttgaggctctgcaactcgactccatgaagtcggaatcgctagtaatc 1323

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 |||||
 Sbjct: 1324 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1383

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 1384 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1443

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 1444 gtgattcat 1452

>gi|22758992|gb|AF534213.1| Uncultured bacterium clone Phe50 16S ribosomal RNA g
 sequence
 Length = 1462

Score = 2428 bits (1225), Expect = 0.0
 Identities = 1395/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Minus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 1457 acgctggcggcaggcctaacacatgcaagtcgagcggtaacacagag-agcttgct-ctc 1400

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |||||
 Sbjct: 1399 gggtagcagcggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 1340

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||||
 Sbjct: 1339 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 1280

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
 |||||
 Sbjct: 1279 gcctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 1220

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 1219 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 1160

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 1159 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 1100

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 1099 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 1040

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 1039 ggcgataagggttaataaccttgatcgattgacgttaccgcgaggaagcaccggctaact 980

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcgttaatcggaattactgggcgta 540
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Sbjct: 979 ccgtgccagcagccgcggttaatacggaggggtgcaagcgttaatcggaattactgggcgta 920

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||
Sbjct: 919 aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 860

Query: 601 gcatttgaaactgggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 859 gcattcgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcgg 800

Query: 661 gaaatgcgtagagatctggaggaataccgggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 799 gaaatgcgtagagatctggaggaataccgggtggcgaaggcgccccctggacaaagactg 740

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 739 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 680

Query: 781 taaacgatgtcgacttggaggttggtgcccttgaggcggtggttccggagctaacgcgtta 840
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Sbjct: 679 taaacgatgtcgacttggaggttggtgcccttgaggcggtggttccggagctaacgcgtta 620

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||||
Sbjct: 619 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 560

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 559 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 500

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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 Sbjct: 499 gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 440

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgggttaagtcgcaacgagcgcaac 1080
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 Sbjct: 439 gcatggctgtcgtcagctcgtgttgtaaagtgggttaagtcgcaacgagcgcaac 380

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
 |||||
 Sbjct: 379 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccagtgataaac 320

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
 |||||
 Sbjct: 319 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 260

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||||
 Sbjct: 259 gctacaatggcgcatataaaagagaagcggaactcgcgagagcaagcggacctcataaagtg 200

Query: 1261 cgtagtagtccggattggagctctgcaactcgactccatgaagtcggaatcgtagtaatc 1320
 |||||
 Sbjct: 199 cgtagtagtccggattggagctctgcaactcgactccatgaagtcggaatcgtagtaatc 140

Query: 1321 gtggatcagaatgccacggtgaatacggtcccgggccttgtagacacaccgcccgtcacacc 1380
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 Sbjct: 139 gtagatcagaatgctacggtgaatacggtcccgggccttgtagacacaccgcccgtcacacc 80

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 79 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 20

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 19 gtgattcat 11

>gi|4581975|emb|AJ233405.1|BNO233405 Buttiauxella noackiae 16S rRNA gene (strain
 Length = 1497

Score = 2422 bits (1222), Expect = 0.0
 Identities = 1396/1451 (96%), Gaps = 6/1451 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggta--acagggagcagcttgctgc 58
 |||||
 Sbjct: 12 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacaggagc---ttgctcc 68

Query: 59 tctgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggat 118

4/22/03

Sbjct: 788 |||||
cgtaaacgatgtcgacttggaggttgttcccttgaggagtggcttccggagctaacgcgt 847

Query: 839 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 898
|||
Sbjct: 848 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 907

Query: 899 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtc 958
|||
Sbjct: 908 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactc 967

Query: 959 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
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Sbjct: 968 ttgacatccacggaattcggcagagatgccttagtgcccttcgggaaccgtgagacaggtg 1027

Query: 1019 ctgcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgca 1078
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Sbjct: 1028 ctgcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgca 1087

Query: 1079 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataa 1138
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Sbjct: 1088 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtgataa 1147

Query: 1139 accggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacac 1198
|||
Sbjct: 1148 actggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacac 1207

Query: 1199 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1258
|||
Sbjct: 1208 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1267

Query: 1259 tgcgtcgtagtcgggattggagtcgcaactcgactccatgaagtcggaatcgctagtaa 1318
|||
Sbjct: 1268 tgcgtcgtagtcgggattggagtcgcaactcgactccgtgaagtcggaatcgctagtaa 1327

Query: 1319 tcgtggatcagaatgccacgggtgaatacgttccccgggccttgtagacacaccgcccgtcaca 1378
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Sbjct: 1328 tcgtagatcagaatgctacgggtgaatacgttccccgggccttgtagacacaccgcccgtcaca 1387

Query: 1379 ccatgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccact 1438
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Sbjct: 1388 ccatgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccact 1447

Query: 1439 ttgtgattcat 1449
|||
Sbjct: 1448 ttgtgattcat 1458

>gi|18419669|gb|AF463533.1| Citrobacter sp. TSA-1 16S ribosomal RNA gene, partial
Length = 1456

Score = 2420 bits (1221), Expect = 0.0

Identities = 1386/1441 (96%)

Strand = Plus / Plus

```
Query: 9      ggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctctgctgacg 68
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Sbjct: 1      ggcaggcctaacacatgcaagtcgaacggtagcacagaggagcttgctccttgggtgacg 60

Query: 69     agtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataactactgga 128
             |||
Sbjct: 61     agtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataactactgga 120

Query: 129    aacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgggcctcatg 188
             |||
Sbjct: 121    aacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgggcctcttg 180

Query: 189    ccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgac 248
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Sbjct: 181    ccatcggatgtgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgac 240

Query: 249    gatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccagact 308
             |||
Sbjct: 241    gatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccagact 300

Query: 309    cctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccatgc 368
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Sbjct: 301    cctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccatgc 360

Query: 369    cgcggtgatgaagaaggccttcggggtgtaaagtactttcagcggggaggaagggtgttgt 428
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Sbjct: 361    cgcggtgatgaagaaggccttcggggtgtaaagtactttcagcggaggaggaaggcattgt 420

Query: 429    ggtaataaaccgcagcaattgacgttaccgcagaagaagcaccgggctaactccgtgcca 488
             |||
Sbjct: 421    ggtaataaaccgcagtgattgacgttactcgcaagaagaagcaccgggctaactccgtgcca 480

Query: 489    gcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgtaaagcgcac 548
             |||
Sbjct: 481    gcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgtaaagcgcac 540

Query: 549    gcaggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaactgcatttga 608
             |||
Sbjct: 541    gcaggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaactgcattccga 600

Query: 609    aactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggtgaaatgcg 668
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Sbjct: 601 aactggcaggctagagtcttgtagaggggggtagaattccagggtgtagcggtgaaatgcg 660

Query: 669 tagagatctggaggaataccggtggcgaaggcggccccctggacgaagactgacgctcag 728
|||||

Sbjct: 661 tagagatctggaggaataccggtggcgaaggcggccccctggacaaagactgacgctcag 720

Query: 729 gtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgccgtaaacgat 788
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Sbjct: 721 gtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgccgtaaacgat 780

Query: 789 gtcgacttgagggttggtcccttgaggcgtggcttccggagctaacgcgttaagtgcacc 848
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Sbjct: 781 gtcgacttgagggttggtcccttgaggcgtggcttccggagctaacgcgttaagtgcacc 840

Query: 849 gcctggggagtagcggccgcaagggttaaaactcaaatgaattgacggggggcccgcacaaagc 908
|||||

Sbjct: 841 gcctggggagtagcggccgcaagggttaaaactcaaatgaattgacggggggcccgcacaaagc 900

Query: 909 ggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtcttgacatcca 968
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Sbjct: 901 ggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactcttgacatcca 960

Query: 969 gagaatcctgcagagatgcgggagtgcccttcgggaactctgagacagggtgctgcatggct 1028
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Sbjct: 961 gagaacttagcagagatgctttggtgccttcgggaactctgagacagggtgctgcatggct 1020

Query: 1029 gtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcgaacccttatcc 1088
|||||

Sbjct: 1021 gtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcgaacccttatcc 1080

Query: 1089 tttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaaccggaggaa 1148
|||||

Sbjct: 1081 tttgttgccagcgggttcggccgggaactcaaaggagactgccagtataaactggaggaa 1140

Query: 1149 ggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgtgctacaat 1208
|||||

Sbjct: 1141 ggtggggatgacgtcaagtcacatcatggcccttacgagtaggggtacacacgtgctacaat 1200

Query: 1209 ggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtcgtag 1268
|||

Sbjct: 1201 ggcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtatgctcgtag 1260

Query: 1269 tccggattggagctctgcaactcgactccatgaaatcggaatcgctagtaatcgtaggatca 1328
|||||

Sbjct: 1261 tccggattggagctctgcaactcgactccatgaaatcggaatcgctagtaatcgtaggatca 1320

Query: 1329 gaatgccacgggtgaatacgttccccgggccttgtagacacaccgcccgtcacaccatgggagt 1388
|||||

Sbjct: 1321 gaatgccacggtgaatacgttccccgggccttgtaacacacgcccgtcacaccatgggagtg 1380

Query: 1389 ggggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccactttgtgattca 1448
 |||||

Sbjct: 1381 ggggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccactttgtgattca 1440

Query: 1449 t 1449

|
 Sbjct: 1441 t 1441

>gi|3282037|emb|Y17663.1|KPY17663 Klebsiella planticola 16S rRNA gene, strain 74
 Length = 1452

Score = 2420 bits (1221), Expect = 0.0
 Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 4 acgctggcggcaggcctaacacatgcaagtcgagcggttagcacagag-agcttgct-ctc 61

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggaggggggataa 120
 | |||||
 Sbjct: 62 ggggtgacgagcggcgacgggtgagtaatgtctgggaaactgcctgatggaggggggataa 121

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||||
 Sbjct: 122 ctactggaaacggtagctaataccgcataacgtcgcaagaccaaagtgggggaccttcgg 181

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
 |||||
 Sbjct: 182 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaaatggctcacc 241

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
 |||||
 Sbjct: 242 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 301

Query: 301 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
 |||||
 Sbjct: 302 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 361

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
 |||||
 Sbjct: 362 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggaggaggaa 421

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
 || |||||
 Sbjct: 422 ggcrttaagggttaataaccttrgygattgacgttactcgcaagaagaagcaccgggctaact 481

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
|||
Sbjct: 482 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 541

Query: 541 aagcgcacgcaggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||
Sbjct: 542 aagcgcacgcaggcggtttgttaagtcagatgtgaaatccccgggctcaacctgggaact 601

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
|||
Sbjct: 602 gcatttgaaactggcaagcttgagtcttgtagaggggggtagaattccagggtgtagcggt 661

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
|||
Sbjct: 662 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacaaagactg 721

Query: 721 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||
Sbjct: 722 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgctg 781

Query: 781 taaacgatgtcgacttggaggttggtcccttgaggcggtggcttccggagctaacgcgtta 840
|||
Sbjct: 782 taaacgatgtcgacttggaggttggtcccttgaggagtggttccggagctaacgcgtta 841

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 900
|||
Sbjct: 842 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 901

Query: 901 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||
Sbjct: 902 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 961

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacagggtgct 1020
|||
Sbjct: 962 gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacagggtgct 1021

Query: 1021 gcatggctgtcgtcagctcgtgttgaaatggtgggttaagtcccgcaacgagcgcaac 1080
|||
Sbjct: 1022 gcatggctgtcgtcagctcgtgttgaaatggtgggttaagtcccgcaacgagcgcaac 1081

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||
Sbjct: 1082 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccagtataaac 1141

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
|||
Sbjct: 1142 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtagggctacacacgt 1201

```

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaaagtg 1260
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Sbjct: 1202 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaaagta 1261

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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Sbjct: 1262 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtacacaccgcccgtcacacc 1380
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Sbjct: 1322 gtagatcagaatgstacggtgaatacgttcccgggccttgtacacaccgcccgtcacacc 1381

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
          |||
Sbjct: 1382 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441 gtgattcat 1449
          |||
Sbjct: 1442 gtgattcat 1450

```

>gi|3282033|emb|Y17659.1|KPY17659 Klebsiella planticola 16S rRNA gene, strain AT
Length = 1452

Score = 2420 bits (1221), Expect = 0.0
Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

```

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
          |||
Sbjct: 4 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagag-agcttgct-ctc 61

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
          |||
Sbjct: 62 gggtagcagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 121

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
          |||
Sbjct: 122 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagtgggggaccttcgg 181

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
          |||
Sbjct: 182 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 241

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
          |||
Sbjct: 242 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 301

```


Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 302 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 361

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 362 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggaggaggaa 421

Query: 421 ggtgttggtgtaataaccgcagcaattgacgttaccgcagaagaagcaccggctaact 480
|| || |||||
Sbjct: 422 ggcrttaaggttaataacyttrgtgattgacgttactcgagaagaagcaccggctaact 481

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
|||||
Sbjct: 482 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 541

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||
Sbjct: 542 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 601

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
|||||
Sbjct: 602 gcatttgaaactggcaagcttgagtcttgtagaggggggtagaattccagggtgtagcggt 661

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcggccccctggacgaagactg 720
|||||
Sbjct: 662 gaaatgcgtagagatctggaggaataccggtggcgaaggcggccccctggacaaagactg 721

Query: 721 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 722 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgctg 781

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||
Sbjct: 782 taaacgatgtcgacttggaggttgttcccttgaggagtggttccggagctaacgcgtta 841

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 900
|||||
Sbjct: 842 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 901

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 902 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 961

Query: 961 gacatccagagaatcctgcagagatgcgggagtgaccttcgggaactctgagacagggtgct 1020
|||||
Sbjct: 962 gacatccagrgaacttagcagagatgctttggtgccttcgggaactctgagacagggtgct 1021

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Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
          |||
Sbjct: 1022 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1081

Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
          |||
Sbjct: 1082 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtataaac 1141

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
          |||
Sbjct: 1142 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1201

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
          |||
Sbjct: 1202 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261 cgtcgtagtccggattggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
          |||
Sbjct: 1262 tgtcgtagtccggattggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
          |||
Sbjct: 1322 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1381

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
          |||
Sbjct: 1382 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441 gtgattcat 1449
          |||
Sbjct: 1442 gtgattcat 1450

```

>gi|21436695|emb|AJ489826.1|UEN489826 Enterobacteriaceae bacterium CF01Ent-1 16S
 CF01Ent-1
 Length = 1483

Score = 2420 bits (1221), Expect = 0.0
 Identities = 1397/1451 (96%), Gaps = 4/1451 (0%)
 Strand = Plus / Plus

```

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacag-ggagcagcttgctgct 59
          |||
Sbjct: 15 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacaggag-agcttgct-ct 72

Query: 60 ctgc-tgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggaggggggat 118
          |||
Sbjct: 73 ctgggtgacgagcggcggacgggtgagtaatgtctgggaaactgcccgatggaggggggat 132

```

Query: 119 aactactggaaacggtagctaataccgcataaacgtctacggaccaaagtgggggaccttc 178
|||
Sbjct: 133 aactactggaaacggtagctaataccgcataaacgtcttcggaccaaagagggggaccttc 192

Query: 179 gggcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctca 238
|||
Sbjct: 193 gggcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaaatggctca 252

Query: 239 cctaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacac 298
|||
Sbjct: 253 cctaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacac 312

Query: 299 ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat 358
|||
Sbjct: 313 ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat 372

Query: 359 gcagccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggagg 418
|||
Sbjct: 373 gcagccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggagg 432

Query: 419 aaggtgttggtgtaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaa 478
|||
Sbjct: 433 aaggcatgaaggttaataacccttagtgattgacgttactcgcagaagaagcaccggctaa 492

Query: 479 ctccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcg 538
|||
Sbjct: 493 ctccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcg 552

Query: 539 taaagcgcacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaa 598
|||
Sbjct: 553 taaagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaa 612

Query: 599 ctgcattgaaactgggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcg 658
|||
Sbjct: 613 ctgcattcgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcg 672

Query: 659 gtgaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacgaagac 718
|||
Sbjct: 673 gtgaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacaaagac 732

Query: 719 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgc 778
|||
Sbjct: 733 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgc 792

Query: 779 cgtaaacgatgtcgacttgaggttggtgcccttgaggcgtggcttccggagctaacgcgt 838
|||
Sbjct: 793 cgtaaacgatgtcgacttgaggttggtgcccttgaggcgtggcttccggagctaacgcgt 852

```

Query: 839  taagtcgaccgcctggggagtagcgccgcaagggttaaaaactcaaattgaattgacgggggc 898
          |||
Sbjct: 853  taagtcgaccgcctggggagtagcggycgcaagggttaaaaactcaaattgaattgacgggggc 912

Query: 899  cgcacaaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtc 958
          |||
Sbjct: 913  cgcacaaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactc 972

Query: 959  ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
          |||
Sbjct: 973  ttgacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtg 1032

Query: 1019 ctgcatggctgtcgtcagctcgtgttgtaaatgttgggttaagtcccgcaacgagcgca 1078
          |||
Sbjct: 1033 ctgcatggctgtcgtcagctcgtgttgtaaatgttgggttaagtcccgcaacgagcgca 1092

Query: 1079 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataa 1138
          |||
Sbjct: 1093 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtgataa 1152

Query: 1139 accggaggaaggtggggatgacgtcaagtcacatgagcccttacgaccagggctacacac 1198
          |||
Sbjct: 1153 actggaggaaggtggggatgacgtcaagtcacatgagcccttacgagtagggctacacac 1212

Query: 1199 gtgctacaatggcgcatacaaagagaagcgacctcgcgagagcaagcggacctcataaag 1258
          |||
Sbjct: 1213 gtgctacaatggcgcatacaaagagaagcgacctcgcgagagcaagcggacctcataaag 1272

Query: 1259 tgcgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaa 1318
          |||
Sbjct: 1273 tgcgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaa 1332

Query: 1319 tcgtggatcagaatgccacggtgaataacgttcccgggccttgtagacacaccgcccgtcaca 1378
          |||
Sbjct: 1333 tcgtagatcagaatgctacggtgaataacgttcccgggccttgtagacacaccgcccgtcaca 1392

Query: 1379 ccatgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1438
          |||
Sbjct: 1393 ccatgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1452

Query: 1439 ttgtgattcat 1449
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Sbjct: 1453 ttgtgattcat 1463

```

>gi|2209046|dbj|AB004754.1| Klebsiella oxytoca gene for 16S ribosomal RNA, parti
 Length = 1441

Score = 2418 bits (1220), Expect = 0.0
Identities = 1389/1443 (96%), Gaps = 2/1443 (0%)
Strand = Plus / Plus

```
Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
             |||
Sbjct: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 58

Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaaactgcctgatggagggggataa 120
             |||
Sbjct: 59     gggtgacgagtgggcgacgggtgagtaatgtctgggaaaactgcctgatggagggggataa 118

Query: 121    ctactggaaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
             |||
Sbjct: 119    ctactggaaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 178

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
             |||
Sbjct: 179    gcctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 238

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 239    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 298

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 299    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 358

Query: 361    agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 359    agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 418

Query: 421    ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 419    ggtgataaggttaataaaccttancaattgacgttaccgcgagaagaagcaccggctaact 478

Query: 481    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
             |||
Sbjct: 479    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 538

Query: 541    aagcgcacgcaggcgggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
             |||
Sbjct: 539    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 598

Query: 601    gcatttgaaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
             |||
Sbjct: 599    gcattcgaaaactggcaggctggagtccttgtagaggggggtagaattccaggtgtagcgg 658
```

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcggccccctggacgaagactg 720
|||||
Sbjct: 659 gaaatgcgtagagatctggaggaataccggtggcgaaggcggccccctggacaaagactg 718

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||
Sbjct: 719 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgctg 778

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||
Sbjct: 779 taaacgatgtcgacttggaggttgttcccttgaggagtggcttccggagctaacgcgtta 838

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatgaattgacggggggccc 900
|||||
Sbjct: 839 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatgaattgacggggggccc 898

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 899 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 958

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
|||||
Sbjct: 959 gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1018

Query: 1021 gcatggctgtcgtcagctcgtgttgaaatggtgggttaagtcccgcaacgagcgcaac 1080
|||||
Sbjct: 1019 gcatggctgtcgtcagctcgtgttgaaatggtgggttaagtcccgcaacgagcgcaac 1078

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Sbjct: 1079 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccagtataaac 1138

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgt 1200
|||||
Sbjct: 1139 tggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtaggggtacacacgt 1198

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
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Sbjct: 1199 gctacaatggcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1258

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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Sbjct: 1259 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1318

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1319 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1378

Query: 1381 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 1379 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1438

Query: 1441 gtg 1443
 |||
 Sbjct: 1439 gtg 1441

>gi|16417818|gb|AF417870.1|AF417870 Pantoea sp. YSS/2001-2 16S ribosomal RNA gen
 Length = 1406

Score = 2416 bits (1219), Expect = 0.0
 Identities = 1342/1383 (97%)
 Strand = Plus / Plus

Query: 67 cgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataactactg 126
 |||||
 Sbjct: 2 cgagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataactactg 61

Query: 127 gaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgggcctca 186
 |||||
 Sbjct: 62 gaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgggcctct 121

Query: 187 tgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacctaggcg 246
 |||||
 Sbjct: 122 tgccatcagatgtgcccagatgggattagctagtagtggtggggtaacggctcacctaggcg 181

Query: 247 acgatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccaga 306
 |||||
 Sbjct: 182 acgatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccaga 241

Query: 307 ctccctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccat 366
 |||||
 Sbjct: 242 ctccctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccat 301

Query: 367 gccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaagggtgtt 426
 |||||
 Sbjct: 302 gccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaagggtgtt 361

Query: 427 gtgggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggtaactccgtgc 486
 |||||
 Sbjct: 362 gaggttaataacctcagcaattgacgttaccgcgagaagaagcaccgggtaactccgtgc 421

Query: 487 cagcagccgcggtaataaccgaggggtgcaagcggttaatcggaattactgggcgtaaagcgc 546
 |||||
 Sbjct: 422 cagcagccgcggtaataaccgaggggtgcaagcggttaatcggaattactgggcgtaaagcgc 481

Query: 547 acgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaactgcattt 606

4/22/03


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      |||
Sbjct: 1202 agtccggattggagctgcaactcgactccatgaagtcggaatcgctagtaatcgtagat 1261

Query: 1327 cagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacaccatggga 1386
      |||
Sbjct: 1262 cagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacaccatggga 1321

Query: 1387 gtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttgtgatt 1446
      |||
Sbjct: 1322 gtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttgtgatt 1381

Query: 1447 cat 1449
      |||
Sbjct: 1382 cat 1384

```

>gi|3282054|emb|Y17669.1|KPY17669 Klebsiella pneumoniae 16S rRNA gene, strain K1
Length = 1452

Score = 2416 bits (1219), Expect = 0.0
Identities = 1391/1449 (95%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

```

Query: 1   acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
      |||
Sbjct: 4   acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagag-agcttgct-ctc 61

Query: 61   tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
      |||
Sbjct: 62   gggtgacgagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 121

Query: 121  ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
      |||
Sbjct: 122  ctactggaaacggtagctaataaccgcataaygtcgcaagaccaaagtgggggaccttcgg 181

Query: 181  gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
      |||
Sbjct: 182  gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 241

Query: 241  taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
      |||
Sbjct: 242  taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 301

Query: 301  tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
      |||
Sbjct: 302  tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 361

Query: 361  agccatgccgcgtgtatgaagaaggccttcggggttgtaaagtactttcagcggggaggaa 420
      |||

```

4/22/03

Sbjct: 1082 ccttatccctttgttgccagcggttcggccgggaactcaaaggagactgccagtgataaac 1141

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
 |||

Sbjct: 1142 tggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1201

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||

Sbjct: 1202 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261 cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||

Sbjct: 1262 tgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 |||

Sbjct: 1322 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1381

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||

Sbjct: 1382 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441 gtgattcat 1449
 |||

Sbjct: 1442 gtgattcat 1450

>gi|6562390|emb|AJ251468.1|EAE251468 Enterobacter aerogenes partial 16S rRNA gen
 Length = 1511

Score = 2416 bits (1219), Expect = 0.0
 Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||
 Sbjct: 4 acgctggcggcaggcctaacacatgcaagtcgagcggtarcacagag-agcttgct-ctc 61

Query: 61 tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |||
 Sbjct: 62 gggtgacgagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 121

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||
 Sbjct: 122 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagtgggggaccttcgg 181

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
 |||
 Sbjct: 182 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaaatgggtcacc 241

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||
Sbjct: 242 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 301

Query: 301 tccagactcctacgggaggcagcagtgagggaatattgcacaatgggcgcaagcctgatgc 360
|||
Sbjct: 302 tccagactcctacgggaggcagcagtgagggaatattgcacaatgggcgcaagcctgatgc 361

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||
Sbjct: 362 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 421

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcagaagaagcaccggctaact 480
|||
Sbjct: 422 ggcgttaagggttaataacccttgccgattgacgttactcgcagaagaagcaccggctaact 481

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
|||
Sbjct: 482 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 541

Query: 541 aagcgcacgcaggcggttgattaagtacagatgtgaaatccccgggctcaacctgggaact 600
|||
Sbjct: 542 aagcgcacgcaggcggtctgtcaagtccgatgtgaaatccccgggctcaacctgggaact 601

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtacgggt 660
|||
Sbjct: 602 gcattcgaaactggcaggctagagtcttgtagaggggggtagaattccagggtgtacgggt 661

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
|||
Sbjct: 662 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacaaagactg 721

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||
Sbjct: 722 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 781

Query: 781 taaacgatgtcgacttgagggttggtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||
Sbjct: 782 taaacgatgtcgacttgagggttggtgcccttgaggcgtggcttccggagctaacgcgtta 841

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||
Sbjct: 842 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 901

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||
Sbjct: 902 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 961

```

Query: 961   gacatccagagaatcctgcagagatgcgggagtccttcgggaactctgagacaggtgct 1020
          |||
Sbjct: 962   gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1021

Query: 1021  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
          |||
Sbjct: 1022  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1081

Query: 1081  ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
          |||
Sbjct: 1082  ccttatcctttgttgccagcgrtycggccgggaactcaaaggagactgccagtataaac 1141

Query: 1141  cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
          |||
Sbjct: 1142  tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtagggctacacacgt 1201

Query: 1201  gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
          |||
Sbjct: 1202  gctacaatggcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261  cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
          |||
Sbjct: 1262  tgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321  gtggatcagaatgccacgggtgaatacgttcccgggacctgtacacaccgcccgtcacacc 1380
          |||
Sbjct: 1322  gtagatcagaatgctacgggtgaatacgttcccgggacctgtacacaccgcccgtcacacc 1381

Query: 1381  atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
          |||
Sbjct: 1382  atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441  gtgattcat 1449
          |||
Sbjct: 1442  gtgattcat 1450

```

>gi|4581974|emb|AJ233404.1|BIZ233404 Buttiiauxella izardii 16S rRNA gene (strain
Length = 1498

Score = 2415 bits (1218), Expect = 0.0
Identities = 1395/1451 (96%), Gaps = 6/1451 (0%)
Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggta--acagggagcagcttgctgc 58
          |||
Sbjct: 12     acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagggagc---ttgctcc 68

```

Query: 59	tctgctgacgagtgggcggaagggtgagtaaatgtctgggaaactgcctgatggagggggat	118
Sbjct: 69	tggg-tgacgagcggcggaagggtgagtaaatgtctgggaaactgcctgatggagggggat	127
Query: 119	aactactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttc	178
Sbjct: 128	aactactggaaacggtagctaataaccgcataacgtcttcggaccaaagagggggaccttc	187
Query: 179	gggcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctca	238
Sbjct: 188	gggcctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaaatggctca	247
Query: 239	cctaggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacac	298
Sbjct: 248	cctaggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacac	307
Query: 299	ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat	358
Sbjct: 308	ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat	367
Query: 359	gcagccatgccgcgtgtatgaagaaggccttcggggttgtaaagtactttcagcggggagg	418
Sbjct: 368	gcagccatgccgcgtgtatgaagaaggccttcggggttgtaaagtactttcagcggggagg	427
Query: 419	aagggtgttggtggttaataaaccgcagcaattgacgttaccgcgagaagaagcaccggctaa	478
Sbjct: 428	aaggcattgtggtggttaataaaccacagtgattgacgttactcgcagaagaagcaccggctaa	487
Query: 479	ctccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcg	538
Sbjct: 488	ctccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcg	547
Query: 539	taaagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaa	598
Sbjct: 548	taaagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaa	607
Query: 599	ctgcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcg	658
Sbjct: 608	ctgcattcgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcg	667
Query: 659	gtgaaatgcgtagagatctggaggaataaccgggtggcgaaggcggccccctggacgaagac	718
Sbjct: 668	gtgaaatgcgtagagatctggaggaataaccgggtggcgaaggcggccccctggacaaaagac	727
Query: 719	tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc	778
Sbjct: 728	tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc	787

Query: 779 cgtaaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgt 838
|||||
Sbjct: 788 cgtaaacgatgtcgacttggaggttgttcccttgaggagtggcttccggagctaacgcgt 847

Query: 839 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 898
|||||
Sbjct: 848 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 907

Query: 899 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtc 958
|||||
Sbjct: 908 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactc 967

Query: 959 ttgacatccagagaatcctgcagagatgcgggagtgccttcgggaactctgagacaggtg 1018
|||||
Sbjct: 968 ttgacatccacggaatttggcagagatgccttagtgcttcgggaacctgagacaggtg 1027

Query: 1019 ctgcatggctgtcgtcagctcgtgttgaaatggtgggttaagtcccgcaacgagcgca 1078
|||||
Sbjct: 1028 ctgcatggctgtcgtcagctcgtgttgaaatggtgggttaagtcccgcaacgagcgca 1087

Query: 1079 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataa 1138
|||||
Sbjct: 1088 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtataa 1147

Query: 1139 accggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacac 1198
|| |||||
Sbjct: 1148 actggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacac 1207

Query: 1199 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1258
|||||
Sbjct: 1208 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1267

Query: 1259 tgcgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaa 1318
|||||
Sbjct: 1268 tgcgtcgtagtcgggatcgagtcctgcaactcgactccgtgaagtcggaatcgctagtaa 1327

Query: 1319 tcgtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1378
|||||
Sbjct: 1328 tcgtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1387

Query: 1379 ccatgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1438
|||||
Sbjct: 1388 ccatgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1447

Query: 1439 ttgtgattcat 1449
|||||
Sbjct: 1448 ttgtgattcat 1458

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

Posted date: Apr 21, 2003 12:40 AM

Number of letters in database: -300,496,531

Number of sequences in database: 1,729,678

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 4,444,676

Number of Sequences: 1729678

Number of extensions: 4444676

Number of successful extensions: 562618

Number of sequences better than 10.0: 94638

Number of HSP's better than 10.0 without gapping: 94564

Number of HSP's successfully gapped in prelim test: 74

Number of HSP's that attempted gapping in prelim test: 29112

Number of HSP's gapped (non-prelim): 463289

length of query: 1449

length of database: 8,289,438,057

effective HSP length: 22

effective length of query: 1427

effective length of database: 8,251,385,141

effective search space: 11774726596207

effective search space used: 11774726596207

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 20 (40.1 bits)